

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: June 30, 2000, 14:52:32 ; Search time 40.56 Seconds  
(without alignments)  
4.088 Million cell updates/sec

Title: US-08-833-506C-120  
Perfect score: 33  
Sequence: 1 QGILERV 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 188963 seqs, 23686106 residues

Total number of hits satisfying chosen parameters: 76368

Minimum DB seq length: 0  
Maximum DB seq length: 15

Post-processing: Minimum Match 0%  
Listing first 100 summaries

Database : A.Geneseq\_36.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	100.0	9	W81272	Human INOS peptide
2	33	100.0	9	W81273	Human INOS peptide
3	33	100.0	12	W81238	Human INOS peptide
4	33	100.0	12	W81301	Human INOS peptide
5	33	100.0	14	W81237	Human INOS peptide
6	33	100.0	14	W81300	Human INOS peptide
7	33	100.0	15	W81233	Human INOS peptide
8	33	100.0	15	W81296	Human INOS peptide
9	29	87.9	8	W81274	Human INOS peptide
10	24	72.7	9	W81239	Human INOS peptide
11	24	72.7	9	W81302	Human INOS peptide
12	23	69.7	9	P33522	Amino acid sequenc
13	23	69.7	10	R33352	Sequence of trypti
14	23	69.7	15	W95122	Peptide X9 express
15	22	66.7	12	W81234	Human INOS peptide
16	22	66.7	12	W81297	Human INOS peptide
17	21	63.6	8	P33513	Amino acid sequenc
18	21	63.6	9	W49676	Human leucocyte an
19	21	63.6	13	P33520	Amino acid sequenc
20	21	63.6	15	W59086	FMDV non-structura
21	20	60.6	5	R62202	CENP-B protein ami
22	20	60.6	7	W66560	Peptide useful as
23	20	60.6	8	R73345	Human TSH receptor
24	20	60.6	8	R73347	Human TSH receptor
25	20	60.6	11	R77218	Mouse anti-human I
26	20	60.6	14	R65049	Random biotinylati
27	20	60.6	14	W11550	FGF9 antigenic pep
28	20	60.6	14	W46652	Biotinylation pep
29	20	60.6	15	P90253	Antigenic peptide
30	19	57.6	4	W46528	Peptide containing
31	19	57.6	6	W87171	Peptide determined
32	19	57.6	7	R71398	VPI peptide used t
33	19	57.6	7	W38293	Poliovirus amino a
34	19	57.6	8	P51212	Analgesic peptide.

35	19	57.6	8	1	R61079	Dynorphin-like pol
36	19	57.6	9	1	R61086	Dynorphin-like pol
37	19	57.6	9	1	R61878	MBP peptide 145, p
38	19	57.6	9	1	R61674	HLA-A2.1 algorithm
39	19	57.6	9	1	R73694	Antigen fragment 1
40	19	57.6	9	1	W01521	Amine-functionaliz
41	19	57.6	11	1	R54763	Plasminogen analog
42	19	57.6	11	1	R61961	MBP peptide 143, p
43	19	57.6	11	1	R67619	Jojoba fatty acyl-
44	19	57.6	13	1	W93441	Staphylococcus aur
45	19	57.6	13	1	W94981	MHC binding peptid
46	19	57.6	14	1	R89867	Cytochrome P450 2C
47	19	57.6	14	1	W64077	Human cytochrome p
48	19	57.6	15	1	R44125	Human myelin basic
49	19	57.6	15	1	R65066	Random biotinylati
50	19	57.6	15	1	R35373	Residues 146-160 o
51	19	57.6	15	1	W05721	Residues 148-162 o
52	19	57.6	15	1	W54678	Peptide from MBP 1
53	19	57.6	15	1	W68579	P. carinii serine
54	19	57.6	15	1	W73606	Human myelin basic
55	18	54.5	6	1	R45221	des-Tyr Dynorphin
56	18	54.5	6	1	R88613	RGD hexapeptide. N
57	18	54.5	6	1	W65973	Dynorphin A (resid
58	18	54.5	7	1	R45210	des-Tyr Dynorphin
59	18	54.5	7	1	R45220	des-Tyr Dynorphin
60	18	54.5	7	1	R91345	Dynorphin A analog
61	18	54.5	7	1	R31336	Dynorphin A analog
62	18	54.5	7	1	W65963	Des-Tyr dynorphin
63	18	54.5	7	1	W65972	Des-Tyr-Gly dynorp
64	18	54.5	7	1	W66555	Peptide useful as
65	18	54.5	7	1	W96295	Vgab peptide fragm
66	18	54.5	8	1	P71269	Sequence of new an
67	18	54.5	8	1	P40299	Proenkephalin, the
68	18	54.5	8	1	P20254	Opitoid peptide 2.
69	18	54.5	8	1	R42485	Peptide 3 from neu
70	18	54.5	8	1	R45209	des-Tyr Dynorphin
71	18	54.5	8	1	R45219	des-Tyr Dynorphin
72	18	54.5	8	1	R60463	Antiproliferative
73	18	54.5	8	1	R61022	Dynorphin-like pol
74	18	54.5	8	1	R38769	Dynorphin-like pol
75	18	54.5	8	1	R61726	PLP peptide 131, p
76	18	54.5	8	1	R61751	MBP peptide 34, po
77	18	54.5	8	1	R91344	Dynorphin A analog
78	18	54.5	8	1	R91335	Dynorphin A analog
79	18	54.5	8	1	W50080	Human chorionic go
80	18	54.5	8	1	W50045	Human beta-hcg pro
81	18	54.5	8	1	W47485	Human beta-hcg pro
82	18	54.5	8	1	W65962	Des-Tyr dynorphin
83	18	54.5	8	1	W65971	Des-Tyr-Gly dynorp
84	18	54.5	8	1	W65556	Peptide useful as
85	18	54.5	8	1	Y01334	E. coli uracil DNA
86	18	54.5	9	1	R27446	ANP receptor agoni
87	18	54.5	9	1	R27447	ANP receptor agoni
88	18	54.5	9	1	R27453	ANP receptor agoni
89	18	54.5	9	1	R27454	ANP receptor agoni
90	18	54.5	9	1	R45208	des-Tyr Dynorphin
91	18	54.5	9	1	R45218	des-Tyr Dynorphin
92	18	54.5	9	1	R61088	Dynorphin-like pol
93	18	54.5	9	1	R61816	PLP peptide 134, p
94	18	54.5	9	1	R73827	Antigen fragment 1
95	18	54.5	9	1	R73819	Antigen fragment 1
96	18	54.5	9	1	R73820	Antigen fragment 1
97	18	54.5	9	1	R73100	Antigen fragment 1
98	18	54.5	9	1	R78913	MAGE 1 38-46 cytot
99	18	54.5	9	1	R91343	Dynorphin A analog
100	18	54.5	9	1	W60481	Tumour homing pept

## ALIGNMENTS

RESULT 1  
W81272

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ID W81272 standard; peptide; 9 AA.
AC W81272; 1999 (first entry)
DE Human iNOS peptide fragment PS-5275.
KW Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;
KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;
KW myocardial infarction; tissue rejection; transplantation; psoriasis;
KW autoimmune disease; multiple sclerosis.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Modified_site 9
FT FT /note= "Val residue amidated"
PN WO9845710-A1.
PD 15-OCT-1998.
PF 11-APR-1997; U06500.
PR 07-APR-1997; US-667777.
PA (WEBB/) WEBBER R.
PI Webber R.
DR WPI: 98-594495/50.
PT Detection of human inducible nitric oxide synthase - using an
PT immunoassay in which a sample is contacted with a specific binding
PT entity reactive with human iNOS or mimics.
PS Example 13; Page 55; 93pp; English.
CC This invention describes an immunoassay method where a sample with a
CC specific binding entity (e.g. a monoclonal antibody) reactive to human
CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used
CC to detect the presence of human iNOS protein in the sample. The method
CC can be used for the detection and quantitation of human iNOS in cells and
CC tissues for various pathophysiological conditions such as sepsis, septic
CC shock, myocardial infarction, rejection of tissue in organs following
CC transplantation, monitoring "flare ups" in certain autoimmune diseases
CC such as lupus, psoriasis, and multiple sclerosis. This sequence
CC represents a peptide from human iNOS which is used in the method of the
CC invention.
SQ Sequence 9 AA;

Query Match 100.0%; Score 33; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.5e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QGILERV 7
Db 3 QGILERV 9

RESULT 3
W81238
ID W81238 standard; peptide; 12 AA.
AC W81238; 1999 (first entry)
DE Human iNOS peptide fragment PS-5227.
KW Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;
KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;
KW myocardial infarction; tissue rejection; transplantation; psoriasis;
KW autoimmune disease; multiple sclerosis.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Modified_site 12
FT FT /note= "Val residue amidated"
PN WO9845710-A1.
PD 15-OCT-1998.
PF 11-APR-1997; U06500.
PR 07-APR-1997; US-667777.
PA (WEBB/) WEBBER R.
PI Webber R.
DR WPI: 98-594495/50.
PT Detection of human inducible nitric oxide synthase - using an
PT immunoassay in which a sample is contacted with a specific binding
PT entity reactive with human iNOS or mimics.
PS Example 4; Page 37; 93pp; English.
CC This invention describes an immunoassay method where a sample with a
CC specific binding entity (e.g. a monoclonal antibody) reactive to human
CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used
CC to detect the presence of human iNOS protein in the sample. The method
CC can be used for the detection and quantitation of human iNOS in cells and
CC tissues for various pathophysiological conditions such as sepsis, septic
CC shock, myocardial infarction, rejection of tissue in organs following
CC transplantation, monitoring "flare ups" in certain autoimmune diseases
CC such as lupus, psoriasis, and multiple sclerosis. This sequence
CC represents a peptide from human iNOS which is used in the method of the
CC invention.
SQ Sequence 12 AA;

Query Match 100.0%; Score 33; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QGILERV 7
Db 5 QGILERV 11

RESULT 4
W81301
ID W81301 standard; peptide; 12 AA.
AC W81301;

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DT 30-APR-1999 (first entry)  
 DE Human iNOS peptide fragment for epitope mapping #22.  
 KW Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;  
 KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;  
 KW myocardial infarction; tissue rejection; transplantation; psoriasis;  
 KW autoimmune disease; multiple sclerosis; epitope mapping.  
 OS Homo sapiens.  
 PN WO9845710-A1.  
 PD 15-OCT-1998.  
 PF 11-APR-1997; U06500.  
 PR 07-APR-1997; US-667777.  
 PA (WEBB/) WEBBER R.  
 PI Webber R;  
 DR WPI; 98-594495/50.  
 PT Detection of human inducible nitric oxide synthase - using an  
 PT immunoassay in which a sample is contacted with a specific binding  
 PT entity reactive with human iNOS or mimics.  
 PS Example 4; Fig 7C; 93pp; English.  
 CC This invention describes an immunoassay method where a sample with a  
 CC specific binding entity (e.g. a monoclonal antibody) reactive to human  
 CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used  
 CC to detect the presence of human iNOS protein in the sample. The method  
 CC can be used for the detection and quantitation of human iNOS in cells and  
 CC tissues for various pathophysiological conditions such as sepsis, septic  
 CC shock, myocardial infarction, rejection of tissue in organs following  
 CC transplantation, monitoring "flare ups" in certain autoimmune diseases  
 CC such as lupus, psoriasis, and multiple sclerosis. This sequence  
 CC represents a peptide from human iNOS which is used in the method of the  
 CC invention. 12 AA;  
 SQ Sequence 12 AA;  
  
 Query Match 100.0%; Score 33; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 0.38; Mismatches 0; Indels 0; Gaps 0;  
 Matches 7; Conservative 0;  
  
 QY 1 QGILERV 7  
 Db 5 QGILERV 11  
 |||||  
  
 RESULT 5  
 W81237  
 ID W81237 standard; peptide; 14 AA.  
 AC W81237;  
 DT 30-APR-1999 (first entry)  
 DE Human iNOS peptide fragment PS-5226.  
 KW Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;  
 KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;  
 KW myocardial infarction; tissue rejection; transplantation; psoriasis;  
 KW autoimmune disease; multiple sclerosis.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT Modified\_site 14 /note= "Gly residue amidated"  
 FT WO9845710-A1.  
 PD 15-OCT-1998.  
 PF 11-APR-1997; U06500.  
 PR 07-APR-1997; US-667777.  
 PA (WEBB/) WEBBER R.  
 PI Webber R;  
 DR WPI; 98-594495/50.  
 PT Detection of human inducible nitric oxide synthase - using an  
 PT immunoassay in which a sample is contacted with a specific binding  
 PT entity reactive with human iNOS or mimics.  
 PS Example 4; Page 37; 93pp; English.  
 CC This invention describes an immunoassay method where a sample with a  
 CC specific binding entity (e.g. a monoclonal antibody) reactive to human  
 CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used  
 CC to detect the presence of human iNOS protein in the sample. The method  
 CC can be used for the detection and quantitation of human iNOS in cells and  
 CC tissues for various pathophysiological conditions such as sepsis, septic  
 CC shock, myocardial infarction, rejection of tissue in organs following

CC transplantation, monitoring "flare ups" in certain autoimmune diseases  
 CC such as lupus, psoriasis, and multiple sclerosis. This sequence  
 CC represents a peptide from human iNOS which is used in the method of the  
 CC invention. 14 AA;  
 SQ Sequence 14 AA;  
  
 Query Match 100.0%; Score 33; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 0.44; Mismatches 0; Indels 0; Gaps 0;  
 Matches 7; Conservative 0;  
  
 QY 1 QGILERV 7  
 Db 5 QGILERV 11  
 |||||  
  
 RESULT 6  
 W81300  
 ID W81300 standard; peptide; 14 AA.  
 AC W81300;  
 DT 30-APR-1999 (first entry)  
 DE Human iNOS peptide fragment for epitope mapping #21.  
 KW Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;  
 KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;  
 KW myocardial infarction; tissue rejection; transplantation; psoriasis;  
 KW autoimmune disease; multiple sclerosis; epitope mapping.  
 OS Homo sapiens.  
 PN WO9845710-A1.  
 PD 15-OCT-1998.  
 PF 11-APR-1997; U06500.  
 PR 07-APR-1997; US-667777.  
 PA (WEBB/) WEBBER R.  
 PI Webber R;  
 DR WPI; 98-594495/50.  
 PT Detection of human inducible nitric oxide synthase - using an  
 PT immunoassay in which a sample is contacted with a specific binding  
 PT entity reactive with human iNOS or mimics.  
 PS Example 4; Fig 7C; 93pp; English.  
 CC This invention describes an immunoassay method where a sample with a  
 CC specific binding entity (e.g. a monoclonal antibody) reactive to human  
 CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used  
 CC to detect the presence of human iNOS protein in the sample. The method  
 CC can be used for the detection and quantitation of human iNOS in cells and  
 CC tissues for various pathophysiological conditions such as sepsis, septic  
 CC shock, myocardial infarction, rejection of tissue in organs following  
 CC transplantation, monitoring "flare ups" in certain autoimmune diseases  
 CC such as lupus, psoriasis, and multiple sclerosis. This sequence  
 CC represents a peptide from human iNOS which is used in the method of the  
 CC invention. 14 AA;  
 SQ Sequence 14 AA;  
  
 Query Match 100.0%; Score 33; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 0.44; Mismatches 0; Indels 0; Gaps 0;  
 Matches 7; Conservative 0;  
  
 QY 1 QGILERV 7  
 Db 5 QGILERV 11  
 |||||  
  
 RESULT 7  
 W81233  
 ID W81233 standard; peptide; 15 AA.  
 AC W81233;  
 DT 30-APR-1999 (first entry)  
 DE Human iNOS peptide fragment PS-5222.  
 KW Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;  
 KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;  
 KW myocardial infarction; tissue rejection; transplantation; psoriasis;  
 KW autoimmune disease; multiple sclerosis.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers



PR 07-APR-1997; US-667777.  
 PA (WEBB/) WEBBER R.  
 PI Webber R;  
 DR WPI: 98-594495/50.  
 PT Detection of human inducible nitric oxide synthase - using an  
 PT immunoassay in which a sample is contacted with a specific binding  
 PT entity reactive with human iNOS or mimics.  
 PS Example 4; Page 37; 93pp; English.  
 CC This invention describes an immunoassay method where a sample with a  
 CC specific binding entity (e.g. a monoclonal antibody) reactive to human  
 CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used  
 CC to detect the presence of human iNOS protein in the sample. The method  
 CC can be used for the detection and quantitation of human iNOS in cells and  
 CC tissues for various pathological conditions such as sepsis, septic  
 CC shock, myocardial infarction, rejection of tissue in organs following  
 CC transplantation, monitoring "flare ups" in certain autoimmune diseases  
 CC such as lupus, psoriasis, and multiple sclerosis. This sequence  
 CC represents a peptide from human iNOS which is used in the method of the  
 CC invention.  
 SQ Sequence 9 AA;

Query Match 72.7%; Score 24; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QGILE 5  
 |||||  
 Db 5 QGILE 9

## RESULT 11

W81302  
 ID W81302 standard; peptide; 9 AA.  
 AC W81302;  
 DT 30-APR-1999 (first entry)  
 DE Human iNOS peptide fragment for epitope mapping #23.  
 DE Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;  
 KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;  
 KW myocardial infarction; tissue rejection; transplantation; psoriasis;  
 KW autoimmune disease; multiple sclerosis; epitope mapping.  
 OS Homo sapiens.  
 PN W09845710-A1.  
 PD 15-OCT-1998.  
 PF 11-APR-1997; U06500.  
 PR 07-APR-1997; US-667777.  
 PA (WEBB/) WEBBER R.  
 PI Webber R;  
 DR WPI: 98-594495/50.  
 PT Detection of human inducible nitric oxide synthase - using an  
 PT immunoassay in which a sample is contacted with a specific binding  
 PT entity reactive with human iNOS or mimics.  
 PS Example 4; Fig 7C; 93pp; English.  
 CC This invention describes an immunoassay method where a sample with a  
 CC specific binding entity (e.g. a monoclonal antibody) reactive to human  
 CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used  
 CC to detect the presence of human iNOS protein in the sample. The method  
 CC can be used for the detection and quantitation of human iNOS in cells and  
 CC tissues for various pathological conditions such as sepsis, septic  
 CC shock, myocardial infarction, rejection of tissue in organs following  
 CC transplantation, monitoring "flare ups" in certain autoimmune diseases  
 CC such as lupus, psoriasis, and multiple sclerosis. This sequence  
 CC represents a peptide from human iNOS which is used in the method of the  
 CC invention.  
 SQ Sequence 9 AA;

Query Match 72.7%; Score 24; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QGILE 5  
 |||||

Db 5 QGILE 9

## RESULT 12

P93522  
 ID P93522 standard; protein; 9 AA.  
 AC P93522;  
 DT 03-JUN-1990 (first entry)  
 DE Amino acid sequence of polylinker region of transfer vector pBF129  
 DE Polylinker protein; silkworm nuclear polyhedrosis virus; NPV;  
 KW HIV gene; gag; pol; SOR; gp120; gp41; polylinker region; pBF129.  
 PN J01074990-A.  
 PD 20-MAR-1989.  
 PF 17-SEP-1987; 231107.  
 PR 17-SEP-1987; JP-231107.  
 PA (MAED) Maeda S.  
 PI  
 DR WPI: 89-127530/17.  
 DR N-PSDB; N92398.  
 PT New transfer vector pBFs, for HIV diagnosis -  
 PT contg. promoter region of polyhedrin protein gene for silkworm  
 PT nuclear polyhedrosis virus deoxyribonucleic acid  
 PS Figure 2; page 9; lipp; Japanese.  
 CC Transfer vectors pBFs were prepd. contg. promoter region of polyhedrin  
 CC protein gene of silkworm nuclear polyhedrosis virus (NPV) recombined  
 CC with HIV gene gag, pol, SOR, gp120 or gp41 in the polylinker region  
 CC of the vector. Thus, HIV antigenic protein can be produced in large  
 CC ams. and used as an antigen for the diagnosis of HIV or for  
 CC vaccine production.  
 SQ Sequence 9 AA;

Query Match 69.7%; Score 23; DB 1; Length 9;  
 Best Local Similarity 66.7%; Pred. No. 1.5e+05;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QGILER 6  
 :|||:|  
 Db 3 EGILDR 8

## RESULT 13

R33352  
 ID R33352 standard; peptide; 10 AA.  
 AC R33352;  
 DT 30-JUN-1993 (first entry)  
 DE Sequence of tryptic peptide derived from purine-rich repeat (GA  
 DE repeat) binding protein (GABP) at peale 1.  
 KW GA binding protein; cis-regulatory element; VP16 mediated induction.  
 OS Synthetic.  
 PN W09304166-A.  
 PD 04-MAR-1993.  
 PF 17-AUG-1991; U06748.  
 PR 16-AUG-1991; US-746032.  
 PA (CARN-) CARNEGIE INST WASHINGTON.  
 PI Lamarco KL, Mc Knight SL, Thompson CC;  
 DR WPI: 93-093998/11.  
 PT DNA encoding GA binding protein sub-unit - allows investigation  
 PT of sub-unit sequence motif functions, for control of rapid cell  
 PT division e.g. in cancer  
 PS Disclosure; Page 3; 68pp; English.  
 CC A cis-regulatory element required for virion associated protein VP16  
 CC mediated induction of herpes simplex virus 1 (HSV1) immediate early  
 CC (IE) genes consists of three imperfect repeats of the purine-rich  
 CC hexanucleotide 5'-CGGAAR-3'. A protein complex capable of avid  
 CC interaction with the purine-rich repeats (GA repeats) has been  
 CC identified in soluble preparations of rat liver nuclei. This GA  
 CC binding protein (GABP) consists of two separable subunits.  
 CC Applicants have isolated cDNA clones encoding both subunits of GABP  
 CC and have revealed that one (GABP alpha) is related to the Ets  
 CC transforming protein, while the other (GABP beta) contains a  
 CC series of 33-amino acid repeats related in sequence to a variety  
 CC of proteins.

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SQ Sequence 10 AA;
Query Match 69.7%; Score 23; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 43;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QGILER 6
   |::|:
Db 5 QGVIEK 10

RESULT 14
W95122
ID W95122 standard; peptide; 15 AA.
AC W95122;
DT 24-MAY-1999 (first entry)
DE Peptide K9 expressed by a modified bacteriophage library.
KW Modified phage library; screening; cell-surface associated protein;
KW therapeutic; diagnostic; disease; ligand; drug; toxin; fractionation;
KW noise elimination; bacteriophage.
OS Bacteriophage ml3.
PN W9906542-A1.
PD 11-FEB-1999.
PF 29-JUL-1998; G02269.
PR 30-JUL-1997; GB-016094.
PA (UNIU ) UNIV GLASGOW.
PI Allen JM, Lavery E;
DR WPI: 99-153772/13.
PT Modified phage display library depleted in phage that react with
PT native cellular proteins - provides reduced noise and higher
PT signal-to-noise ratio when screened against cells transfected to
PT express a specific heterologous protein, used to identify potential
PT therapeutic and diagnostic agents
PS Example 1: Page 29: 49pp; English.
CC The invention relates to a modified phage library for use with a selected
CC strain of cells that have been transformed to express a heterologous
CC protein (I) in a screening procedure, to detect specific binding between
CC individual phage and a recognition site on the heterologous protein. The
CC modified library is produced as follows. The initial phage library is
CC fractionated by contact with strain of cells that do not express (I) to
CC bind any phage that bind to cellular proteins other than the (I). Bound
CC and unbound phages are separated to produce the modified library,
CC depleted in components that bind proteins other than (I). The library is
CC used to identify phage that bind to cell-surface associated (I),
CC specifically receptors. Peptides identified by screening with the
CC modified library are potentially useful as therapeutic and diagnostic
CC agents, for diseases involving (I) or its ligands (including as carriers
CC acid sequences can be used to design other agents for the same uses. The
CC initial fractionation eliminates much of the noise caused by binding to
CC other cell-surface proteins, and the use of transfected cells for
CC screening (these express a far greater number of (I) than wild-type
CC cells) improves the signal-to-noise ratio. The number of rounds of
CC screening may thus be reduced.
SQ Sequence 15 AA;

Query Match 69.7%; Score 23; DB 1; Length 15;
Best Local Similarity 83.3%; Pred. No. 63;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GILERV 7
   |::|:
Db 2 GTLERV 7

RESULT 15
W81234
ID W81234 standard; peptide; 12 AA.
AC W81234;
DT 30-APR-1999 (first entry)
DE Human iNOS peptide fragment PS-5223.

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KW Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;
KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;
KW myocardial infarction; tissue rejection; transplantation; psoriasis;
KW autoimmune disease; multiple sclerosis.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Modified_site 12 /note= "His residue amidated"
PN WO9845710-A1.
PD 15-OCT-1998.
PF 11-APR-1997; U06500.
PR 07-APR-1997; US-667777.
PA (WEBB/) WEBBER R.
PI Webber R;
DR WPI: 98-594495/50.
PT Detection of human inducible nitric oxide synthase - using an
PT immunoassay in which a sample is contacted with a specific binding
PT entity reactive with human iNOS or mimics.
PS Example 4; Page 36; 93pp; English.
CC This invention describes an immunoassay method where a sample with a
CC specific binding entity (e.g. a monoclonal antibody) reactive to human
CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used
CC to detect the presence of human iNOS protein in the sample. The method
CC can be used for the detection and quantitation of human iNOS in cells and
CC tissues for various pathological conditions such as sepsis, septic
CC shock, myocardial infarction, rejection of tissue in organs following
CC transplantation, monitoring "flare ups" in certain autoimmune diseases
CC such as lupus, psoriasis, and multiple sclerosis. This sequence
CC represents a peptide from human iNOS which is used in the method of the
CC invention. 12 AA;
SQ Sequence 12 AA;

Query Match 66.7%; Score 22; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ILERV 7
   |::|:
Db 1 ILERV 5

RESULT 16
W81297
ID W81297 standard; peptide; 12 AA.
AC W81297;
DT 30-APR-1999 (first entry)
DE Human iNOS peptide fragment for epitope mapping #18.
KW Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;
KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;
KW myocardial infarction; tissue rejection; transplantation; psoriasis;
KW autoimmune disease; multiple sclerosis; epitope mapping.
OS Homo sapiens.
PN WO9845710-A1.
PD 15-OCT-1998.
PF 11-APR-1997; U06500.
PR 07-APR-1997; US-667777.
PA (WEBB/) WEBBER R.
PI Webber R;
DR WPI: 98-594495/50.
PT Detection of human inducible nitric oxide synthase - using an
PT immunoassay in which a sample is contacted with a specific binding
PT entity reactive with human iNOS or mimics.
PS Example 4; Fig 7B; 93pp; English.
CC This invention describes an immunoassay method where a sample with a
CC specific binding entity (e.g. a monoclonal antibody) reactive to human
CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used
CC to detect the presence of human iNOS protein in the sample. The method
CC can be used for the detection and quantitation of human iNOS in cells and
CC tissues for various pathological conditions such as sepsis, septic
CC shock, myocardial infarction, rejection of tissue in organs following
CC transplantation, monitoring "flare ups" in certain autoimmune diseases
CC such as lupus, psoriasis, and multiple sclerosis. This sequence

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CC represents a peptide from human INOS which is used in the method of the  
 CC invention.  
 SQ Sequence 12 AA;

Query Match 66.7%; Score 22; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 83;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ILERV 7  
 |||||  
 Db 1 ILERV 5

## RESULT 17

P93513  
 ID P93513 standard; protein; 8 AA.  
 AC P93513;  
 DT 03-JUN-1990 (first entry)  
 DE Amino acid sequence of polylinker region of transfer vector pBF5  
 KW Polylinker protein; silkworm nuclear polyhedrosis virus; NPV;  
 KW HIV gene; gag; pol; SOR; gp120; gp41; polylinker region; pBF5.  
 PN J01074990-A.  
 PD 20-MAR-1989.  
 PF 17-SEP-1987; 231107.  
 PR 17-SEP-1987; JP-231107.  
 PA (MAED) Maeda S.  
 PI  
 DR WPI; 89-127530/17.  
 DR N-PSDB; N92389.  
 PT New transfer vector pBFs, for HIV diagnosis -  
 PT contg. promoter region of polyhedrin protein gene for slink-worm  
 PT nuclear polyhedrosis virus deoxyribonucleic acid  
 PS Figure 2; page 9; 11pp; Japanese.  
 CC Transfer vectors pBFs were prepd. contg. promoter region of polyhedrin  
 CC protein gene of silkworm nuclear polyhedrosis virus (NPV) recombined  
 CC with HIV gene gag, pol, SOR, gp120 or gp41 in the polylinker region  
 CC of the vector. Thus, HIV antigenic protein can be produced in large  
 CC amts. and used as an antigen for the diagnosis of HIV or for  
 CC vaccine production.  
 SQ Sequence 8 AA;

Query Match 63.6%; Score 21; DB 1; Length 8;  
 Best Local Similarity 80.0%; Pred. No. 1.5e+05;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GILER 6  
 |||||  
 Db 3 GILDR 7

## RESULT 18

W49676  
 ID W49676 standard; peptide; 9 AA.  
 AC W49676;  
 DT 05-JUN-1998 (first entry)  
 DE Human leucocyte antigen DQ4 binding peptide #567.  
 KW Human leucocyte antigen; HLA-DQ4; combinatorial library; allergy;  
 KW autoimmune disease.  
 OS Synthetic.  
 PN J08151396-A.  
 PD 11-JUN-1996.  
 PF 28-NOV-1994; 292657.  
 PR 28-NOV-1994; JP-292657.  
 PA (TEIJ) TEIJIN LTD.  
 DR WPI; 96-329479/33.  
 PT HLA-binding oligopeptide and an immuno-regulator contg it - used in  
 PT the treatment of autoimmune disease  
 PS Claim 5; Page 59; 61pp; Japanese.  
 CC This peptide is an example of a peptide which binds to a human leucocyte  
 CC antigen HLA-DQ4 molecule. The peptide was isolated from a phagemid  
 CC combinatorial library comprising the sequence V05953, by screening with

CC an HLA-DQ4 molecule. The peptide is used for the treatment of autoimmune  
 CC disease, especially for treatment of allergies.  
 SQ Sequence 9 AA;

Query Match 63.6%; Score 21; DB 1; Length 9;  
 Best Local Similarity 50.0%; Pred. No. 1.5e+05;  
 Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 GILERV 7  
 |||||  
 Db 1 GVLDR 6

## RESULT 19

P93520  
 ID P93520 standard; protein; 13 AA.  
 AC P93520;  
 DT 03-JUN-1990 (first entry)  
 DE Amino acid sequence of polylinker region of transfer vector pBF81  
 KW Polylinker protein; silkworm nuclear polyhedrosis virus; NPV;  
 KW HIV gene; gag; pol; SOR; gp120; gp41; polylinker region; pBF81.  
 PN J01074990-A.  
 PD 20-MAR-1989.  
 PF 17-SEP-1987; 231107.  
 PR 17-SEP-1987; JP-231107.  
 PA (MAED) Maeda S.  
 PI  
 DR WPI; 89-127530/17.  
 DR N-PSDB; N92396.  
 PT New transfer vector pBFs, for HIV diagnosis -  
 PT contg. promoter region of polyhedrin protein gene for slink-worm  
 PT nuclear polyhedrosis virus deoxyribonucleic acid  
 PS Figure 2; page 9; 11pp; Japanese.  
 CC Transfer vectors pBFs were prepd. contg. promoter region of polyhedrin  
 CC protein gene of silkworm nuclear polyhedrosis virus (NPV) recombined  
 CC with HIV gene gag, pol, SOR, gp120 or gp41 in the polylinker region  
 CC of the vector. Thus, HIV antigenic protein can be produced in large  
 CC amts. and used as an antigen for the diagnosis of HIV or for  
 CC vaccine production.  
 SQ Sequence 13 AA;

Query Match 63.6%; Score 21; DB 1; Length 13;  
 Best Local Similarity 80.0%; Pred. No. 1.5e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GILER 6  
 |||||  
 Db 8 GILDR 12

## RESULT 20

W59086  
 ID W59086 standard; peptide; 15 AA.  
 AC W59086;  
 DT 10-AUG-1998 (first entry)  
 DE FMDV non-structural viral protein immunogenic peptide fragment #14.  
 KW Foot and Mouth disease; FMDV; immunogenic; viral nonstructural protein;  
 KW immunoreactive; antibody; T cell; vaccine; pig; cattle.  
 OS Bos taurus.  
 PN DE19638044-A1.  
 PD 19-MAR-1998.  
 PF 18-SEP-1996; 038044.  
 PR 18-SEP-1996; DE-038044.  
 PA (FARB) BAYER AG.  
 PI Correa R, Froehlich B, Glatthaar-Saalmueller B, Hennen H,  
 PI Pauly T, Pfäffe E, Saalmueller A, Wiesmueller K;  
 DR WPI; 98-180328/17.  
 PT Vaccines against foot and mouth disease virus - comprising peptide  
 PT fragments of nonstructural viral proteins  
 PS Claim 1; Page 14; 27pp; German.  
 CC W59073-W59119 are immunogenic peptides from a foot and mouth disease

CC virus (FMDV) nonstructural protein which are immunoreactive with  
 CC FMDV-specific antibodies or T cells and can be used in vaccines  
 CC against the disease. The vaccines are used especially for immunising  
 CC pigs and cattle.  
 SQ Sequence 15 AA;

Query Match 63.6%; Score 21; DB 1; Length 15;  
 Best Local Similarity 80.0%; Pred. No. 1.7e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GILER 6  
 DB 9 GILER 13  
 |||||

RESULT 21  
 R62202 ID R62202 standard; Protein; 5 AA.  
 AC R62202; 03-MAY-1995 (first entry)  
 DE CNP-B protein amino acids 473-477, homologous to HSV-1 IE motif.  
 KW CNP-B protein; centromere protein; epitope;  
 KW autoantibody; immunoinfective cluster virus; nuclear protein antigen;  
 KW systemic rheumatic disorder; herpes simplex virus; HSV-1 IE;  
 KW immediate early protein; systemic lupus erythematosus; scleroderma.  
 OS Homo sapiens.  
 PN WO9420141-A.  
 PD 15-SEP-1994.  
 PF 10-MAR-1994; U02631.  
 PR 11-MAR-1993; US-029850.  
 PA (UISC-) UNIV SOUTHERN CALIFORNIA.  
 PI Douvas A, Ehresmann G, Takehana Y;  
 DR Methods for treating immunoinfective cluster virus infections -  
 PT utilise antibodies or fragments characteristic of auto antibodies  
 PT produced by patients with rheumatic disorders  
 PS Disclosure; Page 73; 106pp; English.  
 CC A comparison of the CNP-B centromere protein sequence with proteins  
 CC from immunoinfective cluster viruses revealed widespread  
 CC homologues. The importance of these homologous motifs is that they  
 CC are epitopes for autoantibodies occurring in high titres in systemic  
 CC rheumatic disorders. Sera from such patients could be used for  
 CC treatment of immunoinfective cluster virus infections, e.g. HIV-1,  
 CC immunoinfective adenoviruses, human lymphotropic retroviruses,  
 CC rubella virus, CMV and EBV infections.  
 SQ Sequence 5 AA;

Query Match 60.6%; Score 20; DB 1; Length 5;  
 Best Local Similarity 60.0%; Pred. No. 1.5e+05;  
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QGILE 5  
 DB 1 QGVVE 5  
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RESULT 22  
 W66560 ID W66560 standard; peptide; 7 AA.  
 AC W66560; 26-NOV-1998 (first entry)  
 DE Peptide useful as angiogenesis inhibitor.  
 KW anti-angiogenic drug; cancer; arthritis; retinopathy; angiogenesis;  
 KW inhibitor; cancer; arthritis; eye disease; macular degeneration;  
 KW retinopathy.  
 OS Synthetic.  
 FH Key Location/Qualifiers  
 FT Modified\_site 1  
 FT Misc\_difference 3  
 FT /note= "Optional N-terminal acetyl"  
 FT /note= "D-form residue"

FT Modified\_site 7 /note= "Optionally Arg-NH2 or Arg-NHCH2CH3"  
 FT WO9841542-A1.  
 PN 24-SEP-1998.  
 PD 16-MAR-1998; U05327.  
 PR 17-MAR-1997; US-820667.  
 PA (ABBO ) ABBOTT LAB.  
 PA (NOUN ) UNIV NORTHWESTERN.  
 PI Bouck NP, Dawson DW, Henkin J, Schneider AJ;  
 DR WPI; 98-521165/44.  
 PT New peptide(s) containing D-amino acid residues as angiogenesis  
 PT inhibitors - for treatment of e.g. cancer, arthritis, eye diseases  
 PS Example 42; Page 35; 57pp; English.  
 CC The invention relates to peptides of formulae (I)-(IV): T-Gly-Val-D-Ile-  
 CC Thr-Arg-Ile-U (I), V-Gly-D-Val-Ile-D-Thr-D-Arg-D-Ile-W (II), X-D-Arg-D-  
 CC Ile-D-Arg-D-Thr-Ile-D-Val-Y (III), Z-Gly-Val-Ile-Thr-Arg-Ile-U, (IV). T  
 CC is absent or is an N-protecting group or 1-12 amino acids, optionally  
 CC terminated by an N-protecting group; U = Arg or Arg-NR1R2; R1 and R2 =  
 CC hydrogen and 1-4C alkyl; V and X are absent or N-protecting groups.  
 CC W = D-Arg or D-Arg-NR1R2; Y = Gly or Gly-NR1R2; Z = 1-12 amino acids,  
 CC optionally terminated by a protecting group and including at least one  
 CC D-amino acid. The peptides are inhibitors of angiogenesis (they inhibit  
 CC migration of endothelial cells) and are useful for treatment of cancer,  
 CC arthritis, psoriasis, infections of, or surgical injury to, the eye,  
 CC macular degeneration or diabetic retinopathy. They can also be used  
 CC for treating other autoimmune or ocular diseases, blood vessel disease,  
 CC angiofibroma, wound granulation, etc. The present sequence represents an  
 CC example of an angiogenesis inhibitor disclosed in the specification.  
 SQ Sequence 7 AA;

Query Match 60.6%; Score 20; DB 1; Length 7;  
 Best Local Similarity 33.3%; Pred. No. 1.5e+05;  
 Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 GILERV 7  
 DB 1 GVIKRI 6  
 |:::|

RESULT 23  
 R73346 ID R73346 standard; Peptide; 8 AA.  
 AC R73346; 12-DEC-1995 (first entry)  
 DE Human TSH receptor (residues 291-298).  
 KW thyroid stimulating hormone receptor; TSH; human; Homo sapiens;  
 KW antibody; affinity; detection.  
 OS Synthetic.  
 PN J07089991-A.  
 PD 04-APR-1995.  
 PF 28-SEP-1993; 240853.  
 PR 28-SEP-1993; JP-240853.  
 PA (MTP ) MITSUBISHI PETROCHEMICAL CO LTD.  
 DR WPI; 95-167251/22.  
 PT Novel polypeptide(s) having affinity for the human TSH receptor  
 PT antibody - used in detection of the TSH antibody.  
 PS Example 1; Page 25; 54pp; Japanese.  
 CC Peptides with affinity to human TSH (thyroid stimulating hormone)  
 CC receptor antibody are used for detection of the antibody. (See also  
 CC R73201-592).  
 SQ Sequence 8 AA;

Query Match 60.6%; Score 20; DB 1; Length 8;  
 Best Local Similarity 80.0%; Pred. No. 1.5e+05;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QGILE 5  
 DB 3 RGILE 7  
 :|||



## RESULT 24

R73347 ID R73347 standard; Peptide; 8 AA.  
 AC R73347;  
 DE 12-DEC-1995 (first entry)  
 DT Human TSH receptor (residues 293-300).  
 KW thyroid stimulating hormone receptor; TSH; human; Homo sapiens;  
 KW antibody; affinity; detection.  
 OS Synthetic.  
 PN J07089991-A.  
 PD 04-APR-1995.  
 PF 28-SEP-1993; 240853.  
 PR 28-SEP-1993; JP-240853.  
 PA (MTP ) MITSUBISHI PETROCHEMICAL CO LTD.  
 DR WPI: 95-167251/22.  
 PT Novel polypeptide(s) having affinity for the human TSH receptor  
 PT antibody - used in detection of the TSH antibody.  
 PS Example 1; Page 25; 54pp; Japanese.  
 CC Peptides with affinity to human TSH (thyroid stimulating hormone)  
 CC receptor antibody are used for detection of the antibody. (See also  
 CC R73201-592)  
 SQ Sequence 8 AA;

Query Match 60.6%; Score 20; DB 1; Length 8;  
 Best Local Similarity 80.0%; Pred. No. 1.5e+05;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

## QY 1 QGILE 5

Db 1 RGILE 5

## RESULT 25

R77218 ID R77218 standard; Peptide; 11 AA.

AC R77218;  
 DE 23-AUG-1995 (first entry)  
 DT Mouse anti-human IL-6 Ab H chain V region framework region 4.  
 KW Primer; PCR; amplification; kappa; light chain; variable region; mouse; human;  
 KW Interleukin; antibody; hybridoma; CDR; framework; constant region;  
 KW heavy chain; disorder; antigenicity.  
 OS Synthetic.  
 PN W09428159-A.  
 PD 08-DEC-1994.  
 PF 30-MAY-1994; J00859.  
 PR 31-MAY-1993; JP-129787.  
 PA (CHUS ) CHUGAI SEIYAKU KK.  
 PA (CHUS ) CHUGAI PHARM CO LTD.  
 PI Hirata Y, Sato K, Tsuchiya M;  
 DR WPI: 95-022828/03.  
 PT Antibody against IL-6 - useful for the therapy and treatment of  
 PT IL-6 related disorders.  
 PS Claim 13; Page 66; 82pp; Japanese.  
 CC The sequence of the mouse anti-human interleukin-6 (IL-6) antibody heavy  
 CC chain variable region framework region (FR) 4. The sequences of FR1-4  
 CC (R77215-8) were used in conjunction with the complementarity determining  
 CC regions 1-3 (R77212-4) to construct a chimaeric antibody against human  
 CC interleukin-6 (IL-6). The vectors Q75914-7 express constructs encoding  
 CC fragments of a chimaeric antibody to the human IL-6 comprising (a) a  
 CC light chain with (i) a variable region containing 3 CDR (R77201-3)  
 CC inserted into several framework regions (FR) (R77204-7) and (ii) a human  
 CC light chain constant region and (b) a heavy chain with (i) a variable  
 CC region containing 3 CDR (R77212-4) inserted into FR (R77215-8) and (ii)  
 CC a human light chain constant region. The FR of the light chain may be  
 CC mouse derived (Q75888) or from the human antibody REI. The heavy chain  
 CC FR may also be mouse derived (Q75889) or from the human antibody DAW.  
 CC The antibodies can be used in the treatment of IL-6 related disorders.  
 CC The antibodies are useful as they have low antigenicity due to the use of  
 CC human derived sequences and low antigenicity mouse derived sequences.  
 SQ Sequence 11 AA;

Query Match 60.6%; Score 20; DB 1; Length 14;  
 Best Local Similarity 80.0%; Pred. No. 2.6e+02;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

## QY 1 QGILE 5

Db 2 QGIFE 6

## RESULT 27

W11550 ID W11550 standard; Peptide; 14 AA.

AC W11550;  
 DT 19-SEP-1997 (first entry)  
 DE FGF9 antigenic peptide, SP32.  
 KW Mouse; chicken; fibroblast growth factor 9; FGF9; detection;  
 KW fibroblast growth factor receptor 3; FGFR3; cartilage repair;  
 KW bone repair; antagonist; anti-FGF9 antibody; endochondromas;  
 KW solitary hereditary exostosis; multiple hereditary exostosis;  
 KW hallux valgus deformity; achondroplasia; synovial chondromatosis.  
 OS Synthetic.  
 PN W09641523-A1.  
 PD 27-DEC-1996.  
 PF 12-JUN-1996; IL0011.  
 PR 12-JUN-1995; US-000137.  
 PA (YEDA ) YEDA RES & DEV CO LTD.  
 PI Yayon A;  
 DR WPI: 97-065215/06.  
 PT Medical and diagnostic use of fibroblast growth factor 9 - and

Query Match 60.6%; Score 20; DB 1; Length 11;  
 Best Local Similarity 71.4%; Pred. No. 2e+02;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

## QY 1 QGILERV 7

Db 3 QGILVTV 9

## RESULT 26

R65049 ID R65049 standard; Peptide; 14 AA.

AC R65049;  
 DT 24-OCT-1995 (first entry)  
 DE Random biotinylation peptide 17.  
 KW biotinylation; peptide; recombinant; fusion protein; small;  
 KW specific; defined; purification; Biotin; enzyme; biotin.  
 OS Synthetic.  
 FH Key Location/Qualifiers  
 FT modified\_site 9 /note= "biotin-Lys"  
 PN W09504069-A.  
 PD 09-FEB-1995.  
 PR 28-JUL-1994; U08538.  
 PR 30-JUL-1993; US-099991.  
 PA (AFFY-) AFFYMAX TECHNOLOGIES NV.  
 PI Schatz PJ;  
 DR WPI: 95-090609/12.  
 PT Production of biotinylated proteins by expression of a  
 PT recombinant DNA vector - which encodes a fusion protein  
 PT comprising a protein and a biotinylated peptide.  
 PS Claim 10; Page 136; 146pp; English.  
 CC A library of small, efficient peptide biotinylation sequences (R65048-66)  
 CC was generated by using a generic peptide (R65047) and a system known as  
 CC the "peptides on plasmids" system. At some positions in the sequences,  
 CC no clear consensus is apparent. At other residues, however, clear trends  
 CC emerge. A protein can be biotinylated by constructing a recombinant DNA  
 CC expression vector encoding a fusion protein, comprising a protein and a  
 CC biotinylation peptide. A host cell, eg. E. coli is transformed with the  
 CC vector and is cultured in the presence of biotin and a biotinylation  
 CC enzyme, eg. Biotin.  
 SQ Sequence 14 AA;

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PT recombinant fibroblast growth factor 9 DNA
PS Example 1; Page 7; 32pp; English.
CC The sequences given in W11549-50 represent antigenic peptide fragments
CC of fibroblast growth factor 9 (FGF9) which were used in the production
CC of anti-FGF9 antibodies. FGF9 is used in the method of the invention
CC for detecting fibroblast growth factor receptor 3 (FGFR3) in a sample
CC or tissue. The method comprises contacting the sample or tissue with
CC FGF9, allowing formation of receptor-ligand pairs, and detecting any
CC FGFR3-FGF9 pairs. Compositions containing FGF9 can be used to increase
CC FGFR3 activity, esp. to stimulate cartilage or bone repair. Compositions
CC containing FGF9 antagonists or FGF9 binding agents (e.g. anti-FGF9
CC antibodies) can be used to treat diseases caused by an excess of FGF9
CC or overactivity of FGFR3, esp. multiple or solitary hereditary exostosis,
CC hallux valgus deformity, achondroplasia, synovial chondromatosis and
CC endochondromas.
SQ Sequence 14 AA;

Query Match 60.6%; Score 20; DB 1; Length 14;
Best Local Similarity 66.7%; Pred. No. 2.6e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QGILER 6
Db 4 KGILRR 9
:||||

RESULT 28
W46652
ID W46652 standard; peptide; 14 AA.
AC W46652;
DE 28-MAY-1998 (first entry)
DT Biotinylation peptide isolated from random library 2.
DW Biotinylation peptide; biotinylation enzyme; biotin-protein ligase;
KW BIRA; biotin ligase; biotin; purification; immobilisation; labelling;
KW detection; protein.
OS Synthetic.
PN US5723584-A.
PD 03-MAR-1998.
PF 03-FEB-1995; 383753.
PR 30-JUL-1993; US-099991.
PA (AFFY-) AFFYMAX TECHNOLOGIES NV.
PI Schatz PJ;
DR WPI; 98-178542/16.
PT Peptide(s) that can be biotinylated by biotin ligase - and fusion
PT proteins containing them
PS Claim 3; Column 66; 33pp; English.
CC Peptides W46651-69 are non-naturally occurring biotinylation peptides,
CC derived from a library constructed to express peptides of the generic
CC sequence W46650. The library was constructed using oligonucleotides
CC V16121-23. The peptides contain a biotinylatable sequence motif,
CC recognised by a biotinylation enzyme, e.g. biotin-protein ligase (BIRA).
CC The C or N terminus of the peptides can be covalently coupled to a
CC protein that is incapable of being biotinylated by a biotin ligase.
CC The peptides can be biotinylated in vitro or in vivo, especially with
CC BIRA biotin ligase, and used for the purification, immobilisation,
CC labelling or detection of proteins.
SQ Sequence 14 AA;

Query Match 60.6%; Score 20; DB 1; Length 14;
Best Local Similarity 80.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QGILE 5
Db 2 QGIFE 6
|||||

RESULT 29
P90253
ID P90253 standard; peptide; 15 AA.
AC P90253;

PT 26-FEB-1990 (first entry)
DE Antigenic peptide for detecting, inhibiting and neutralising HIV-1.
KW HIV-1; antigenic determinants.
OS HIV-1.
PN EP-330359-A.
PD 30-AUG-1989.
PF 14-FEB-1989; 301364.
PR 25-FEB-1988; US-160378.
PA (BIRA) Bio Rad Labs Inc.
PI Walker RP; Parekh BS;
DR WPI; 89-250452/35.
DE New peptide(s) for detecting, inhibiting and neutralising HIV-1
DE corres. to antigenic determinants encoded by conserved regions
DE of HIV-1 genome.
PS Disclosure; page 4; 16pp; English.
CC Peptide is one of several fragments from gp 120 and gp41 (env gene)
CC p18 and p24 (gag gene), p32 (pol gene) and proteins encoded by the
CC tat, orf trs/art and sor genes. They are used for detecting,
CC inhibiting and neutralising HIV-1 infection. Dosage is pref.
CC 5-25 mg/kg. The peptides can be used for any type of immunological
CC detection esp. dot blot and ELISA.
CC See also P90191-P90274.
SQ Sequence 15 AA;

Query Match 60.6%; Score 20; DB 1; Length 15;
Best Local Similarity 60.0%; Pred. No. 2.7e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QGILE 5
Db 1 QGVVE 5
||::|

RESULT 30
W46528
ID W46528 standard; peptide; 4 AA.
AC W46528;
DE 20-MAY-1998 (first entry)
DT Peptide containing a protease binding site.
DW Protease binding site; protease; protease indicator; fluorescent signal;
KW detection; protease activity.
OS Synthetic.
PN US5714342-A.
PD 03-FEB-1998.
PF 27-OCT-1995; 549008.
PR 27-OCT-1995; US-549008.
PR 28-OCT-1994; US-331383.
PA (ONCO-) ONCOIMMUNIN INC.
PI Komoriya A, Packard BS;
DR WPI; 98-158345/14.
DE Fluorogenic substrates for protease determination - having two
DE closely spaced fluorophores flanking protease binding site
DE Disclosure; Column 4; 39pp; English.
CC Peptides W46520-53 contain protease binding sites. They are used to
CC produce novel reagents whose fluorescence increases in the presence of
CC particular proteases. These fluorogenic protease indicators (substrates)
CC provide a high intensity fluorescent signal at a visible wavelength when
CC they are digested by a protease. The fluorogenic indicators have the
CC general formula:
CC F1--C1--P--C2--F2
CC | |
CC (S1)n (S2)k
CC where:
CC P is a peptide containing a protease binding site, e.g. W46520-53.
CC F1 and F2 are fluorophores.
CC S1 and S2 are peptide spacers e.g. W46554-58.
CC n, k = 0 or 1.
CC C1 and C2 are conformation-determining regions that introduce a bend
CC into the composition which positions the fluorophores adjacent to each
CC other with a separation of less than 100 Angstrom.
CC When n is 1, S1 is joined to the terminal alpha-amino group of C1 by a
CC peptide bond, and when k is 1, S2 is joined to the terminal carboxy group

```

CC of C2 by a peptide bond. The protease indicators are used for detecting  
 CC protease activity in a biological sample. The sample is contacted with  
 CC the indicator and any change in fluorescence is detected, an increase in  
 CC fluorescence indicating protease activity.  
 SQ Sequence 4 AA;

Query Match 57.6%; Score 19; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 OGIL 4  
 ||||  
 Db 1 OGIL 4

Search completed: June 30, 2000, 14:52:36  
 Job time: 6003 sec

***This Page Blank (uspto)***

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: June 30, 2000, 14:54:15 ; Search time 50.08 seconds  
(without alignments)  
8.195 Million cell updates/sec

Title: US-08-833-506c-120

Perfect score: 33

Sequence: 1 QGILERV 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 168808 seqs, 58629743 residues

Total number of hits satisfying chosen parameters: 2577

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Listing first 100 summaries

Database :

PIR\_63:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	63.6	15	2 PA0076	fructose-bisphosph
2	19	57.6	14	2 S50900	chlorophyll a/b-bi
3	19	57.6	14	2 S35267	acetyl-CoA carboxy
4	18	54.5	9	2 PH0942	T-cell receptor be
5	18	54.5	15	2 A53085	lipid transfer pro
6	17	51.5	15	2 PS0382	Ig heavy chain J r
7	16	48.5	13	2 S09018	hemolytic protein
8	16	48.5	14	2 A59018	MUCL enhancer bind
9	15	45.5	10	2 S19296	16K protein - poul
10	15	45.5	13	2 I58003	hprt protein - Chi
11	15	45.5	14	2 S29789	hypothetical prote
12	15	45.5	14	2 S03530	Ig heavy chain J r
13	15	45.5	14	2 S65392	cytochrome-c oxida
14	15	45.5	15	2 PA0075	fructose-bisphosph
15	15	45.5	15	2 PA0102	fructose-bisphosph
16	15	45.5	15	2 PH1377	T antigen variant
17	14	42.4	7	2 PT0246	Ig heavy chain CRD
18	14	42.4	10	2 S06964	hypothetical prote
19	14	42.4	10	2 B56899	serum heterodimer
20	14	42.4	11	1 XASNEA	bradykinin-potenti
21	14	42.4	11	2 A61483	pyridoxal kinase (
22	14	42.4	11	2 S34065	ornithine decarbox
23	14	42.4	12	2 B58503	outer membrane por
24	14	42.4	12	2 C33099	148K exoantigen -
25	14	42.4	12	2 PH1467	T-cell receptor be
26	14	42.4	12	2 H41946	T-cell receptor ga
27	14	42.4	12	4 JX0315	aminotransferase c
28	14	42.4	13	2 S66235	sperm motility inh
29	14	42.4	14	2 S66234	sperm motility inh
30	14	42.4	14	2 C44823	synaptosomal-assoc

31	14	42.4	15	1 LFTWL	leu leader peptide
32	14	42.4	15	2 S21240	alpha-glucosidase
33	14	42.4	15	2 A28497	neurotensin-relate
34	14	42.4	15	2 D48394	major fat-globule
35	14	42.4	15	2 I40665	ILVN leader pepti
36	14	42.4	15	2 PN0629	integration host f
37	14	42.4	15	2 T09463	ribosomal protein
38	14	42.4	15	2 PA0071	superoxide dismuta
39	14	42.4	15	2 S05700	insulin-like growt
40	14	42.4	15	2 S05699	insulin-like growt
41	14	42.4	15	2 B56046	urinary tract ston
42	14	42.4	15	2 PH0806	T-cell receptor al
43	14	42.4	15	2 S17214	gap junction prote
44	13	39.4	4	2 E44823	synaptosomal-assoc
45	13	39.4	5	2 PT0278	Ig heavy chain CRD
46	13	39.4	8	2 T10077	hypothetical prote
47	13	39.4	10	2 JQ0943	hypothetical 1.3K
48	13	39.4	10	2 F44644	neurotoxin-associa
49	13	39.4	10	2 I44644	neurotoxin-associa
50	13	39.4	11	2 S47020	trigger factor hom
51	13	39.4	11	2 B41835	translation elonga
52	13	39.4	11	2 PH0903	T-cell receptor be
53	13	39.4	11	4 I54081	retinoic acid rece
54	13	39.4	12	2 B46662	collagen alpha 2(V
55	13	39.4	12	2 B56049	urinary tract ston
56	13	39.4	12	2 A42324	cytochrome P450c27
57	13	39.4	13	1 JZVHP1	crabrolin - Europe
58	13	39.4	13	2 S22889	lp9B protein - Shi
59	13	39.4	13	2 G44644	neurotoxin-associa
60	13	39.4	13	2 S14316	photosystem I 9K c
61	13	39.4	13	2 S09716	2S albumin large c
62	13	39.4	13	2 H44957	protein P18 - comm
63	13	39.4	13	2 S09019	hemolytic protein
64	13	39.4	13	2 A57789	gallbladder stone
65	13	39.4	14	2 JN0390	histamine-releasin
66	13	39.4	14	2 I54945	gene C protein - E
67	13	39.4	14	2 C39170	acyl-lacyl-carrier
68	13	39.4	14	2 PA0015	seed storage prote
69	13	39.4	14	2 A61306	ribonuclease M (EC
70	13	39.4	14	2 S58426	spermathecin AWN h
71	13	39.4	14	2 PH1639	Ig H chain V-D-J r
72	13	39.4	15	2 S26791	Ig heavy chain V r
73	13	39.4	15	2 A43298	myosin, gizzard -
74	13	39.4	15	2 S43321	RNA-binding protei
75	13	39.4	15	2 PQ0750	self-incompatibili
76	13	39.4	15	2 A61522	7.5k surfactant-as
77	13	39.4	15	2 F57789	gallbladder stone
78	13	39.4	15	2 B33527	fructose-2,6-bisph
79	13	39.4	15	2 S62675	collagen type I -
80	13	39.4	15	2 PH1590	Ig H chain V-D-J r
81	13	39.4	15	2 PT0096	pyruvate dehydroge
82	13	39.4	15	2 PH1455	T-cell receptor al
83	12	36.4	6	2 S11024	hydrogensulfite re
84	12	36.4	6	2 A49792	acylaminoacyl-pept
85	12	36.4	7	2 I54257	phenylalanine hydr
86	12	36.4	8	2 S20162	leghemoglobin III
87	12	36.4	8	2 A54823	olfactory receptor
88	12	36.4	8	2 B54823	olfactory receptor
89	12	36.4	9	2 A60427	beta-neoendorphin
90	12	36.4	10	2 A60410	seed storage prote
91	12	36.4	10	2 C38925	ferredoxin--NADP+
92	12	36.4	10	2 PA0116	ferredoxin--NADP+
93	12	36.4	10	2 PS0220	cytochrome P450 (1
94	12	36.4	10	2 S17048	carnitine medium/1
95	12	36.4	10	2 A61354	kinase activator p
96	12	36.4	10	2 S29190	probable antigen 5
97	12	36.4	11	2 E41476	ribosomal protein
98	12	36.4	11	2 PC4267	gene HEXA protein
99	12	36.4	11	2 PN0167	
100	12	36.4	12	2 I64829	

ALIGNMENTS

RESULT 1  
PA0076  
fructose-bisphosphate aldolase (EC 4.1.2.13) - fungus (Fusarium sporotrichioides) (fragment)  
C:Species: Fusarium sporotrichioides  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 20-Feb-1995  
C:Accession: PA0076  
R:Chow, L.P.; Fukaya, N.; Sugiyura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.  
submitted to JIPID, October 1994  
A:Reference number: PA0051  
A:Accession: PA0076  
A:Molecule type: protein  
A:Residues: 1-15 <KHO>  
C:Keywords: aldehyde-lyase; carbon-carbon lyase

Query Match 63.6%; Score 21; DB 2; Length 15;  
Best Local Similarity 66.7%; Pred. No. 1.3e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 OGILER 6  
||: ||  
Db 5 OGLKER 10

RESULT 2  
S50900  
chlorophyll a/b-binding protein Lhcb5 - spinach (fragment)  
N:Alternate names: light-harvesting complex LHCIIc protein  
C:Species: Spinacia oleracea (spinach)  
C:Date: 19-Mar-1997 #sequence\_revision 23-Apr-1999 #text\_change 23-Apr-1999  
C:Accession: S50900  
R:Walters, R.G.; Ruban, A.V.; Horton, P.  
Eur. J. Biochem. 226, 1063-1069, 1994  
A:Title: Higher plant light-harvesting complexes LHCIIa and LHCIIc are bound by dicyclohexylphosphoribosylated Lhcb5  
A:Reference number: S50900; MUID:95112835  
A:Accession: S50900  
A:Molecule type: protein  
A:Residues: 1-14 <WAL>  
C:Superfamily: chlorophyll a/b-binding protein  
C:Keywords: chlorophyll; chloroplast; light-harvesting complex; photosynthesis; photosynthesis

Query Match 57.6%; Score 19; DB 2; Length 14;  
Best Local Similarity 60.0%; Pred. No. 3.7e+02;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GILER 6  
||: ||  
Db 6 GLLDR 10

RESULT 3  
S35267  
acetyl-CoA carboxylase (EC 6.4.1.2) - wheat (fragment)  
C:Species: Triticum aestivum (common wheat)  
C:Date: 19-Mar-1997 #sequence\_revision 24-Mar-1999 #text\_change 24-Mar-1999  
C:Accession: S35267  
R:Gornicki, P.; Haselkorn, R.  
Plant Mol. Biol. 22, 547-552, 1993  
A:Title: Wheat acetyl-CoA carboxylase.  
A:Reference number: S35267; MUID:93320392  
A:Accession: S35267  
A:Molecule type: protein  
A:Residues: 1-14 <GOR>  
A:Experimental source: leaf  
C:Function:  
A:Description: catalyzes the ATP-dependent carboxylation of acetyl-CoA to malonyl-CoA  
A:Pathway: fatty acid biosynthesis  
C:Keywords: fatty acid biosynthesis; ligase

Query Match 57.6%; Score 19; DB 2; Length 14;  
Best Local Similarity 60.0%; Pred. No. 3.7e+02;  
Matches 2; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 OGILERV 7  
||: ||  
Db 4 KGVKKV 10

RESULT 4  
PH0942  
T-cell receptor beta chain V-D-J region (clone 13) - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 30-May-1997  
C:Accession: PH0942  
R:Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.  
J. Exp. Med. 174, 1467-1476, 1991  
A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allelism  
A:Reference number: PH0942; MUID:92078857  
A:Accession: PH0942  
A:Molecule type: mRNA  
A:Residues: 1-9 <GOL>  
A:Experimental source: complete Freund's adjuvant-immunized lymph node  
A:Note: the authors translated the codon TGC for residue 2 as Ala  
C:Keywords: T-cell receptor

Query Match 54.5%; Score 18; DB 2; Length 9;  
Best Local Similarity 60.0%; Pred. No. 1.7e+03;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 OGILE 5  
||: ||  
Db 3 KGLLE 7

RESULT 5  
A53085  
lipid transfer protein - rabbit (fragment)  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 13-Sep-1994 #sequence\_revision 18-Nov-1994 #text\_change 23-Mar-1995  
C:Accession: A53085  
R:Ko, K.W.; Oikawa, K.; Ohnishi, T.; Kay, C.M.; Yokoyama, S.  
Biochemistry 32, 6729-6736, 1993  
A:Title: Purification, characterization, and conformational analysis of rabbit plasma  
A:Reference number: A53085; MUID:93320050  
A:Accession: A53085  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-15 <ROL>  
A:Experimental source: plasma  
A:Note: sequence extracted from NCBI backbone (NCBIP:135263)

Query Match 54.5%; Score 18; DB 2; Length 15;  
Best Local Similarity 50.0%; Pred. No. 6.7e+02;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GILERV 7  
||: ||  
Db 10 GIVXRI 15

RESULT 6  
PS0382  
Ig heavy chain J region 2 - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 06-Jun-1997  
C:Accession: PS0382  
R:Lang, P.; Mocikat, R.  
Gene 102, 261-264, 1991  
A:Title: Immunoglobulin heavy-chain joining genes in the rat: comparison with mouse a  
A:Reference number: JH0666; MUID:91340162

A;Accession: PS0382  
A:Molecule type: DNA  
A:Residues: 1-15 <LAN>  
A;Cross-references: EMBL:X56791  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin

Query Match 51.5%; Score 17; DB 2; Length 15;  
Best Local Similarity 42.9%; Pred. No. 1.2e+03; Indels 0; Gaps 0;  
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 QGILERV 7  
| | | | |  
Db 7 QGVHVT 13

RESULT 7  
S09018  
hemolytic protein A1 - edible frog (fragment)  
C;Species: Rana esculenta (edible frog)  
C;Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 18-Jun-1993  
C;Accession: S09018  
R;Simmaco, M.; De Biase, D.; Severini, C.; Alta, M.; Erspamer, G.F.; Barra, D.; Bossa, F.  
Biochim. Biophys. Acta 1033, 318-323, 1990  
A;Title: Purification and characterization of bioactive peptides from skin extracts of R.  
A;Reference number: S09018; MUID:90198965  
A;Accession: S09018  
A:Molecule type: protein  
A;Residues: 1-13 <SIM>

Query Match 48.5%; Score 16; DB 2; Length 13;  
Best Local Similarity 50.0%; Pred. No. 1.7e+03; Indels 0; Gaps 0;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GILERV 7  
| | | | |  
Db 7 GILSQL 12

RESULT 8  
A59018  
MUC1 enhancer binding protein 70K chain MUC1EBP-70 - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 08-May-1998 #sequence\_revision 08-May-1998 #text\_change 08-May-1998  
C;Accession: A59018

R;Abe, M.; Smith, C.J.; Larson, C.J.  
submitted to the Protein Sequence Database, May 1998  
A;Description: Involvement of "Ku-like" proteins in the transcription of MUC1/DF3, a bre  
A;Reference number: A59018  
A;Accession: A59018  
A:Molecule type: protein  
A;Residues: 1-14 <ABE>  
A;Experimental source: breast cancer cell line MCF-7  
A;Note: 3-Val was also found  
C;Keywords: DNA binding; heterodimer

Query Match 48.5%; Score 16; DB 2; Length 14;  
Best Local Similarity 66.7%; Pred. No. 1.8e+03; Indels 0; Gaps 0;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QGILERV 6  
| | | | |  
Db 9 QGILEK 14

RESULT 9  
S19296  
16K protein - poulard wheat  
C;Species: Triticum turgidum (poulard wheat)  
C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 24-Jul-1997

C;Accession: S19296  
R;Sanchez-Monge, R.; Gomez, L.; Barber, D.; Lopez-Otin, C.; Armentia, A.; Salcedo, G.  
Biochem. J. 281, 401-405, 1992  
A;Title: Wheat and barley allergens associated with baker's asthma. Glycosylated subu  
A;Reference number: S19296; MUID:92143804  
A;Accession: S19296  
A;Status: preliminary  
A:Molecule type: protein  
A;Residues: 1-10 <SAN>

Query Match 45.5%; Score 15; DB 2; Length 10;  
Best Local Similarity 50.0%; Pred. No. 2.2e+03; Indels 0; Gaps 0;  
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 GILE 5  
| | | | |  
Db 7 GLME 10

RESULT 10  
I58003  
hpvt protein - Chinese hamster (fragment)  
C;Species: Crictetus griseus (Chinese hamster)  
C;Date: 19-Mar-1997 #sequence\_revision 07-Nov-1997 #text\_change 14-Nov-1997  
C;Accession: I58003  
R;Fusco, J.C.; Zimmerman, L.J.; Fekete, A.; Setzer, R.W.; Rossiter, B.J.  
Mutat. Res. 289, 171-183, 1992  
A;Title: Analysis of X-ray-induced HPRT mutations in CHO cells: insertion and deletio  
A;Reference number: I58003; MUID:93024555  
A;Accession: I58003  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A;Residues: 1-13 <RES>  
A;Cross-references: GB:S46270; NID:g257049  
C;Genetics:  
A;Gene: hpvt

Query Match 45.5%; Score 15; DB 2; Length 13;  
Best Local Similarity 75.0%; Pred. No. 2.9e+03; Indels 0; Gaps 0;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 LERV 7  
| | | | |  
Db 1 LEKV 4

RESULT 11  
S29789  
hypothetical protein - Thermoplasma acidophilum (fragment)  
C;Species: Thermoplasma acidophilum  
C;Date: 25-Feb-1994 #sequence\_revision 26-May-1995 #text\_change 26-May-1995  
C;Accession: S29789  
R;Bright, J.R.; Byrom, D.; Danson, M.J.; Hough, D.W.; Townner, P.  
Eur. J. Biochem. 211, 549-554, 1993  
A;Title: Cloning, sequencing and expression of the gene encoding glucose dehydrogenas  
A;Reference number: S29788; MUID:93170285  
A;Accession: S29789  
A;Status: preliminary  
A:Molecule type: DNA  
A;Residues: 1-14 <BRI>  
A;Cross-references: EMBL:X59788

Query Match 45.5%; Score 15; DB 2; Length 14;  
Best Local Similarity 40.0%; Pred. No. 3.1e+03; Indels 0; Gaps 0;  
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 ILERV 7  
| | | | |  
Db 4 LLKRI 8

RESULT 12  
S03530  
Ig heavy chain J region (JH-4) - African clawed frog  
C:Species: Xenopus laevis (African clawed frog)  
C:Date: 21-Nov-1993 #sequence\_revision 08-Nov-1996 #text\_change 09-Sep-1997  
C:Accession: S03530  
R:Schwager, J.; Grossberger, D.; du Pasquier, L.  
EMBO J. 7, 2409-2415, 1988  
A:Title: Organization and rearrangement of immunoglobulin M genes in the amphibian Xenopus laevis  
A:Reference number: S01159; MUID:89052653  
A:Accession: S03530  
A:Molecule type: DNA  
A:Residues: 1-14 <SCH>  
A:Cross-references: EMBL:X14918; NID:g64805; PID:el6056; PID:g1334657

Query Match 45.5%; Score 15; DB 2; Length 14;  
Best Local Similarity 57.1%; Pred. No. 3.1e+03;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QGILERV 7  
||| |  
Db 6 QGTLVTV 12

RESULT 13  
S65392  
cytochrome-c oxidase (EC 1.9.3.1) chain VIII-L - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 12-Feb-1998 #sequence\_revision 20-Feb-1998 #text\_change 07-May-1999  
C:Accession: S65392; S65393; S65391  
R:Schaeffer, H.; Noack, H.; Halangk, W.; Brandt, U.; von Jagow, G.  
Eur. J. Biochem. 230, 235-241, 1995  
A:Title: Cytochrome-c oxidase in developing rat heart. Enzymic properties and amino-term  
A:Reference number: S65372; MUID:95324529  
A:Accession: S65392  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-14 <SCH>  
A:Accession: S65393  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-14 <SC2>  
A:Accession: S65391  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-14 <SC3>  
C:Keywords: oxidoreductase

Query Match 45.5%; Score 15; DB 2; Length 14;  
Best Local Similarity 50.0%; Pred. No. 3.1e+03;  
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 GILE 5  
|||  
Db 11 GVLD 14

RESULT 14  
PA0075  
fructose-bisphosphate aldolase (EC 4.1.2.13) I - fungus (Fusarium sporotrichioides) (fra  
N:Alternate names: aldolase; fructose-1,6,-bisphosphate triosephosphate-lase  
C:Species: Fusarium sporotrichioides  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 10-Nov-1995  
C:Accession: PA0075; PA0077  
R:Chow, L.P.; Fukaya, N.; Sugitara, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.  
submitted to JIPID, October 1994  
A:Reference number: PA0051  
A:Accession: PA0075  
A:Molecule type: protein  
A:Residues: 1-15 <CHO>

Query Match 45.5%; Score 15; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QGI 3  
|||  
Db 1 QGI 3

RESULT 17  
PT0246  
Ig heavy chain CRD3 region (clone 2-103D) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
C:Accession: PT0246  
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

A:Note: this form (I) had a molecular weight of 30.6K and an isoelectric point of 5.3  
A:Accession: PA0077  
A:Molecule type: protein  
A:Residues: 1-15 <CH2>  
A:Note: this form (II) had a molecular weight of 31.6K and an isoelectric point of 5.  
C:Keywords: aldehyde-lyase; carbon-carbon lyase

Query Match 45.5%; Score 15; DB 2; Length 15;  
Best Local Similarity 50.0%; Pred. No. 3.3e+03;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QGILER 6  
| : | |  
Db 3 QEVLSR 8

RESULT 15  
PA0102  
fructose-bisphosphate aldolase (EC 4.1.2.13) III - fungus (Fusarium sporotrichioides)  
C:Species: Fusarium sporotrichioides  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 03-Mar-1995  
C:Accession: PA0102  
R:Chow, L.P.; Fukaya, N.; Sugitara, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.  
submitted to JIPID, October 1994  
A:Reference number: PA0051  
A:Accession: PA0102  
A:Molecule type: protein  
A:Residues: 1-15 <CHO>  
C:Keywords: aldehyde-lyase; carbon-carbon lyase

Query Match 45.5%; Score 15; DB 2; Length 15;  
Best Local Similarity 50.0%; Pred. No. 3.3e+03;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QGILER 6  
| : | |  
Db 3 QEVLSR 8

RESULT 16  
PH1377  
T antigen variant K-5 - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999  
C:Accession: PH1377  
R:Lill, N.L.; Judith Tevethia, M.; Hendrickson, W.G.; Tevethia, S.S.  
J. Exp. Med. 176, 449-457, 1992  
A:Title: Cytotoxic T lymphocytes (CTL) against a transforming gene product select for  
A:Reference number: PH1373  
A:Accession: PH1377  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-15 <LIL>

Query Match 45.5%; Score 15; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QGI 3  
|||  
Db 1 QGI 3



J. Exp. Med. 173, 395-407, 1991  
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and  
A:Reference number: PT0222; MUID:91108337  
A:Accession: PT0246  
A:Molecule type: DNA  
A:Residues: 1-7 <YAM>  
A:Experimental source: B lymphocyte  
C:Keywords: heterotetramer; immunoglobulin

Query Match 42.4%; Score 14; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. NO. 1.7e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GIL 4  
|:|:  
Db 5 GIL 7

RESULT 18  
S06964  
hypothetical protein (nifa 5' region) - Rhizobium leguminosarum (fragment)  
C:Species: Rhizobium leguminosarum  
C:Date: 22-Jan-1993 #sequence\_revision 22-Jan-1993 #text\_change 08-Oct-1999  
C:Accession: S06964  
R:Roelink, P.W.; Hontelez, J.G.J.; van Kammen, A.; van den Bos, R.C.  
Mol. Microbiol. 3, 1441-1447, 1989  
A:Title: Nucleotide sequence of the regulatory nifa gene of Rhizobium leguminosarum PRE:  
A:Reference number: S06964; MUID:90136072  
A:Accession: S06964  
A:Molecule type: DNA  
A:Residues: 1-10 <ROE>  
A:Cross-references: EMBL:X17073; NID:g46208; PIDN:CAA34923.1; PID:g809748

Query Match 42.4%; Score 14; DB 2; Length 10;  
Best Local Similarity 50.0%; Pred. NO. 3.8e+03;  
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 GILE 5  
|:|:  
Db 5 GVLK 8

RESULT 19  
B56899  
serum heterodimer, 24K chain - sandbar shark (fragment)  
C:Species: Carcharhinus plumbeus (sandbar shark)  
C:Date: 11-Aug-1995 #sequence\_revision 11-Aug-1995 #text\_change 11-Aug-1995  
C:Accession: B56899  
R:Vazquez-Moreno, L.; Porath, J.; Schluter, S.F.; Marchalonis, J.J.  
Comp. Biochem. Physiol. B Comp. Biochem. 103, 563-568, 1992  
A:Title: Purification of a novel heterodimer from shark (Carcharhinus plumbeus) serum by  
A:Reference number: A56899; MUID:93092592  
A:Accession: B56899  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-10 <VAZ>  
C:Keywords: glycoprotein; plasma

Query Match 42.4%; Score 14; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. NO. 3.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ERV 7  
|:|:  
Db 5 ERV 7

RESULT 20  
XASNBA  
bradykinin-potentiating peptide B - mamushi

C:Species: Aqkistrodon blomhoffi (mamushi)  
C:Date: 13-Jul-1981 #sequence\_revision 13-Jul-1981 #text\_change 08-Dec-1995  
C:Accession: A01254  
R:Kato, H.; Suzuki, T.  
Proc. Jpn. Acad. 46, 176-181, 1970  
A:Reference number: A01254  
A:Accession: A01254  
A:Molecule type: protein  
A:Residues: 1-11 <KAT>  
A:Note: the sequence of the natural peptide was confirmed by the synthesis and analysis  
C:Superfamily: bradykinin-potentiating peptide  
C:Keywords: angiotensin-converting enzyme inhibitor; bradykinin; pyroglutamic acid; v  
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 42.4%; Score 14; DB 1; Length 11;  
Best Local Similarity 50.0%; Pred. NO. 4.2e+03;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 OGILR 6  
|:|:  
Db 1 QGLPPR 6

RESULT 21  
A61483  
pyridoxal kinase (EC 2.7.1.35) - sheep (fragment)  
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C:Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 07-Oct-1994  
C:Accession: A61483  
R:Churchich, J.E.  
J. Protein Chem. 9, 613-621, 1990  
A:Title: Cleavage of pyridoxal kinase into two structural domains: kinetics of proteo  
A:Reference number: A61483; MUID:91197387  
A:Accession: A61483  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-11 <CHU>  
C:Keywords: homodimer; phosphotransferase

Query Match 42.4%; Score 14; DB 2; Length 11;  
Best Local Similarity 50.0%; Pred. NO. 4.2e+03;  
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 ILER 6  
|:|:  
Db 8 VLQR 11

RESULT 22  
S34065  
ornithine decarboxylase - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Dec-1993 #sequence\_revision 10-Nov-1995 #text\_change 07-May-1999  
C:Accession: S34065  
R:Tsirka, S.E.; Turck, C.W.; Coffino, P.  
Biochem. J. 293, 289-295, 1993  
A:Title: Multiple active conformers of mouse ornithine decarboxylase.  
A:Reference number: S34065; MUID:93319524  
A:Accession: S34065  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-11 <TSI>

Query Match 42.4%; Score 14; DB 2; Length 11;  
Best Local Similarity 50.0%; Pred. NO. 4.2e+03;  
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 LERV 7  
|:|:  
Db 7 LDRI 10

```
RESULT 23
B58503
outer membrane porin protein OprD homolog - unidentified bacterium (fragment)
N:Alternate names: 43K bile stone protein
C:Species: unidentified bacterium
C>Date: 07-Feb-1997 #sequence_revision 07-Feb-1997 #text_change 10-Jul-1998
C:Accession: B58503
submitted to the Protein Sequence Database, October 1996
R:Binette, J.P.; Binette, M.B.
A:Description: The proteins of kidney and gallbladder stones.
A:Reference number: A58501
A:Accession: B58503
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-12 <BIN>
A:Experimental source: human bile with stones
A>Note: sequenced along with secondary sequence MXIGVNEXL

Query Match 42.4%; Score 14; DB 2; Length 12;
Best Local Similarity 40.0%; Pred. No. 4.5e+03;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QGILE 5
Db 7 KGFIE 11

RESULT 24
C33099
148K exoantigen - Plasmodium falciparum (fragment)
C:Species: Plasmodium falciparum
C>Date: 24-Aug-1990 #sequence_revision 24-Aug-1990 #text_change 18-Aug-1992
C:Accession: C33099
R:Nichols, J.H.; Hager, L.P.
submitted to the Protein Sequence Database, May 1990
A:Reference number: A33098
A:Accession: C33099
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-12 <NIC>

Query Match 42.4%; Score 14; DB 2; Length 12;
Best Local Similarity 66.7%; Pred. No. 4.5e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QGI 3
Db 3 QGV 5

RESULT 25
PH1467
T-cell receptor beta chain (clone 223/27) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 11-Apr-1995
C:Accession: PH1467
R:Casanova, J.L.; Martison, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; K
J. Exp. Med. 177, 811-820, 1993
A:Title: T cell receptor selection by and recognition of two class I major histocompatib
A:Reference number: PH1430; MUID:93171821
A:Accession: PH1467
A:Molecule type: mRNA
A:Residues: 1-12 <CAS>
A:Experimental source: cytolytic T-lymphocyte
C:Superfamily: immunoglobulin homology
C:Keywords: receptor; T-cell

Query Match 42.4%; Score 14; DB 2; Length 12;
```

```
Best Local Similarity 66.7%; Pred. No. 4.5e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QGI 3
Db 7 QGV 9

RESULT 26
H41946
T-cell receptor gamma chain (5t.12) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C:Accession: H41946
R:Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
Mol. Cell. Biol. 11, 5902-5909, 1991
A:Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma
A:Reference number: H41946; MUID:92049316
A:Accession: H41946
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-12 <WHE>
C:Keywords: T-cell receptor

Query Match 42.4%; Score 14; DB 2; Length 12;
Best Local Similarity 66.7%; Pred. No. 4.5e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QGI 3
Db 5 QGV 7

RESULT 27
JX0315
aminotransferase chimera DX18 - synthetic (fragment)
C:Species: synthetic
C>Date: 28-May-1999 #sequence_revision 28-May-1999 #text_change 28-May-1999
C:Accession: JX0315
R:Miyazawa, K.; Kawaguchi, S.; Okamoto, A.; Kato, R.; Ogawa, T.; Kuramitsu, S.
J. Biochem. 115, 568-577, 1994
A:Title: Construction of aminotransferase chimeras and analysis of their substrate sp
A:Reference number: JX0315; MUID:94334304
A:Accession: JX0315
A:Molecule type: DNA
A:Residues: 1-12 <MIY>
C:Comment: This enzyme is a chimeric enzyme of Escherichia coli aspartate aminotransf
C:Comment: The parental enzymes catalyze the reversible amino group transfer reaction
C:Keywords: aminotransferase

Query Match 42.4%; Score 14; DB 4; Length 12;
Best Local Similarity 50.0%; Pred. No. 4.5e+03;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ILER 6
Db 9 LMER 12

RESULT 28
S66235
sperm motility inhibitor protein - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C:Accession: S66235
R:Iwamoto, T.; Hiroaki, H.; Furuichi, Y.; Wada, K.; Satoh, M.; Osada, T.;
FEBS Lett. 368, 420-424, 1995
A:Title: Cloning of boar SPWI gene which is expressed specifically in seminal vesicle
A:Reference number: S66233; MUID:95361914
A:Accession: S66235
A>Status: preliminary
```

A:Molecule type: protein  
A:Residues: 1-13 <IWA>  
A:Note: Pro-6 was also found

Query Match 42.4%; Score 14; DB 2; Length 13;  
Best Local Similarity 50.0%; Pred. No. 4.9e+03;  
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 GILE 5  
|:|:  
Db 10 GVLK 13

RESULT 29  
S66234  
sperm motility inhibitor protein - pig (fragment)  
C:Species: Sus scrofa domestica (domestic pig)  
C>Date: 14-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 13-Mar-1997  
C:Accession: S66234  
R:Iwamoto, T.; Hiroaki, H.; Furuichi, Y.; Wada, K.; Satoh, M.; Osada, T.; Gage  
FES Lett. 368, 420-424, 1995  
A:Title: Cloning of boar SPMI gene which is expressed specifically in seminal vesicle an  
A:Reference number: S66233; MUID:95361914  
A:Accession: S66234  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-14 <IWA>  
A:Note: Phe-9 and Phe-12 were also found

Query Match 42.4%; Score 14; DB 2; Length 14;  
Best Local Similarity 50.0%; Pred. No. 5.3e+03;  
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 GILE 5  
|:|:  
Db 11 GVLK 14

RESULT 30  
C44823  
synaptosomal-associated protein SNAP-25 peptide 8 - rabbit (fragment)  
N:Alternate names: superprotein peptide 8  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C>Date: 31-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 15-Jun-1996  
C:Accession: C44823  
R:Loewy, A.; Liu, W.S.; Baitinger, C.; Willard, M.B.  
J. Neurosci. 11, 3412-3421, 1991  
A:Title: The major 35S-methionine-labeled rapidly transported protein (superprotein) is  
A:Reference number: A44823; MUID:9204785  
A:Accession: C44823  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-14 <LOE>  
A:Experimental source: visual tissue  
A:Note: sequence extracted from NCBI backbone (NCBIP:64253)  
C:Keywords: membrane trafficking

Query Match 42.4%; Score 14; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 5.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LER 6  
|:|:  
Db 12 LER 14

Search completed: June 30, 2000, 14:54:17  
Job time: 5182 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: June 30, 2000, 19:03:14 ; Search time 39.08 seconds  
(without alignments)

5.455 Million cell updates/sec

Title: US-08-833-506c-120

Perfect score: 33

Sequence: 1 QGILERV 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 83857 seqs, 30454973 residues

Total number of hits satisfying chosen parameters: 668

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Listing first 100 summaries

Database : SwissProt\_38.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	60.6	15	ATP2_PINPS	P81663 pinus pinas
2	16	48.5	13	HPAI_RANES	P32415 rana escule
3	16	48.5	13	NUPM_HUMAN	P51970 homo sapien
4	15	45.5	14	YGDH_THEAC	Q05213 thermoplas
5	15	45.5	15	CDN2_LITGI	P56247 litoria gil
6	14	42.4	10	TRP5_LEUMA	P81737 leucophaea
7	14	42.4	11	BPPB_AGRHA	P01021 agkistrodon
8	14	42.4	12	CD11_LITXA	P56245 litoria xan
9	14	42.4	12	CD14_LITXA	P56246 litoria xan
10	14	42.4	13	CHEP_PARID	P42718 parapolybia
11	14	42.4	13	FIBB_HYLLA	P14472 hylobates l
12	14	42.4	14	FIBB_MANLE	P14474 mandrillus
13	14	42.4	14	MI14_EISFO	P46979 eisenia foe
14	14	42.4	14	UN37_CLOPA	P81358 clostridium
15	14	42.4	15	LPL_THETH	P21234 thermus aqu
16	14	42.4	15	MALT_BACTO	P80072 bacillus th
17	13	39.4	12	PA2B_VIPBO	P31859 vipera beru
18	13	39.4	12	UP01_CAEEL	P55954 caenorhabdi
19	13	39.4	13	CRBL_VESCR	P01518 vespa crabr
20	13	39.4	13	FARB_ASCSU	P43173 ascaris suu
21	13	39.4	13	HPB9_RANES	P32416 rana escule
22	13	39.4	14	CRBL_VESOR	P17236 vespa orien
23	13	39.4	14	IF2G_RAT	P81795 rattus norv
24	13	39.4	14	MI14_PHEVI	P46980 pheretima v
25	12	36.4	6	ACPB_RABIT	P25154 oryctolagus
26	12	36.4	10	CU30_LOCOMI	P11735 locusta mig
27	12	36.4	10	TRP9_LEUMA	P81741 leucophaea
28	12	36.4	10	UFAL_HUMAN	P32118 homo sapien
29	12	36.4	11	CH60_DROME	P35380 drosophila
30	12	36.4	13	CRBL_ICASP	P17237 icaria sp.
31	12	36.4	13	CRBL_VESAN	P17233 vespa anali
32	12	36.4	13	CRBL_VESLE	P17235 vespa lew
33	12	36.4	13	CRBL_VESMA	P17232 vespa manda
34	12	36.4	13	CRBL_VESTR	P17231 vespa tropi

35	12	36.4	13	1	CRBL_VESXA	P17234 vespa xanth
36	12	36.4	13	1	UN12_CLOPA	P81353 clostridium
37	12	36.4	13	1	UVRD_SALTY	Q05311 salmonella
38	12	36.4	14	1	ALYT_ALYOB	P08944 alytes obst
39	12	36.4	14	1	SCK3_LEIQU	P45661 leitoria gil
40	12	36.4	15	1	CDN3_LITGI	P56248 litoria gil
41	11	33.3	7	1	UH11_RAT	P56576 rattus norv
42	11	33.3	8	1	ANG2_BOTJA	Q10592 bothrops ja
43	11	33.3	8	1	LCK3_LEUMA	P21142 leucophaea
44	11	33.3	9	1	OXYT_RAJCL	P42994 raja clavata
45	11	33.3	9	1	THYF_PIG	P01255 sus scrofa
46	11	33.3	9	1	ULAE_HUMAN	P31931 homo sapien
47	11	33.3	10	1	ANGL_BOTJA	Q10581 bothrops ja
48	11	33.3	10	1	ANGT_BOVIN	P01017 bos taurus
49	11	33.3	10	1	ANGT_CHICK	P01018 gallus gall
50	11	33.3	10	1	BPP_VIPAS	P31351 vipera aspi
51	11	33.3	10	1	SPI_HAURO	Q10997 halocynthia
52	11	33.3	11	1	BPP4_BOTIN	P30424 bothrops in
53	11	33.3	11	1	BPP_AGRHP	P04562 agkistrodon
54	11	33.3	11	1	CEP1_ACHFU	P22790 achatina fu
55	11	33.3	11	1	HS70_PINPS	P81672 pinus pinas
56	11	33.3	11	1	UN05_CLOPA	P81350 clostridium
57	11	33.3	12	1	TM2A_METMA	P80632 methanosarc
58	11	33.3	13	1	BOML_PSEGU	P42991 pseudophryn
59	11	33.3	13	1	BPP1_BOTJA	P01020 bothrops ja
60	11	33.3	13	1	LPAA_PORGI	P81411 porphyromon
61	11	33.3	13	1	YCIA_SALTY	P25944 salmonella
62	11	33.3	14	1	ANGT_HORSE	P01016 equus cabal
63	11	33.3	14	1	MAST_POLJA	P01517 polistes ja
64	11	33.3	14	1	MAST_VESXA	P01515 vespa xanth
65	11	33.3	15	1	COXI_THUOB	P80978 thunnus obe
66	11	33.3	15	1	LMA2_LOCOMI	P38497 locusta mig
67	11	33.3	15	1	METK_MAIZE	P80616 zea mays (m
68	11	33.3	15	1	PLAS_MICAE	P10625 microcystis
69	11	33.3	15	1	SCOT_RAT	P01159 rattus norv
70	11	33.3	15	1	UC25_MAIZE	P80631 zea mays (m
71	11	33.3	15	1	URE2_MORMO	P17338 morganella
72	10	30.3	8	1	COXG_RAT	P80430 rattus norv
73	10	30.3	8	1	NS3_MYCTU	P81152 mycobacteri
74	10	30.3	8	1	UH09_RAT	P56575 rattus norv
75	10	30.3	9	1	FIBB_PAPAN	P19344 papio anubi
76	10	30.3	9	1	FIBB_PAPHA	P19343 papio hamad
77	10	30.3	9	1	FIBB_THEGE	P19342 theropitheci
78	10	30.3	9	1	TAL1_PICJA	P17440 pichia jadi
79	10	30.3	9	1	TAL3_PICJA	P17441 pichia jadi
80	10	30.3	9	1	ULAK_MOUSE	P99031 mus musculu
81	10	30.3	10	1	PAP1_PARMA	P81863 pardachirus
82	10	30.3	10	1	TKN1_SCYCA	P08608 scyllorhinu
83	10	30.3	10	1	TKNB_CHICK	P19851 gallus gall
84	10	30.3	10	1	TKNB_ONCMY	P28500 oncorhynch
85	10	30.3	10	1	TKNB_RANCA	P22689 rana catesb
86	10	30.3	10	1	TKNB_RANRI	P29135 rana ridibu
87	10	30.3	10	1	TKNC_RANCA	P22690 rana catesb
88	10	30.3	10	1	TKNK_PIG	P01292 sus scrofa
89	10	30.3	10	1	TKN_PHYBI	P08610 phyllomedus
90	10	30.3	10	1	TKS1_AEDAE	P42634 aedes aegyp
91	10	30.3	10	1	TKS2_AEDAE	P42635 aedes aegyp
92	10	30.3	10	1	UP11_CAEEL	P55956 caenorhabdi
93	10	30.3	10	1	XYNB_DICB4	P80717 dictyoglomu
94	10	30.3	11	1	ANGT_CRIGE	P09037 crinia geor
95	10	30.3	11	1	PVK_PERAM	P41837 periplaneta
96	10	30.3	11	1	TKN1_PSEGU	P42986 pseudophryn
97	10	30.3	11	1	TKN1_UPERU	P08612 uperoleia r
98	10	30.3	11	1	TKN2_PSEGU	P42987 pseudophryn
99	10	30.3	11	1	TKN2_UPERU	P08616 uperoleia r
100	10	30.3	11	1	TKN3_PSEGU	P42988 pseudophryn

ALIGNMENTS

RESULT\_1  
ATP2\_PINPS

ID ATP2\_PINPS STANDARD; PRT; 15 AA.  
AC P81663;  
DT 15-JUL-1999 (Rel. 38, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 15-FEB-2000 (Rel. 39, Last annotation update)  
DE ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL (EC 3.6.1.34) (FRAGMENT).  
GN ATPB.  
OS Pinus pinaster (Maritime pine).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC euphyllophytes; Spermatophyta; Coniferopsida; Coniferales; Pinaceae;  
OC Pinus.  
RN [1]  
RP SEQUENCE.  
RC TISSUE-NEEDLE;  
RX MEDLINE; 93274088.  
RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,  
RA Frigerio J.-M., Plomion C.;  
RT "Separation and characterization of needle and xylem maritime pine  
RT proteins.";  
RL Electrophoresis 20:1098-1108(1999).  
CC -!- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON  
CC GRADIENT ACROSS THE MEMBRANE. THE BETA CHAIN IS THE CATALYTIC  
CC SUBUNIT (BY SIMILARITY).  
CC -!- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC  
CC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE  
CC SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)  
CC HAS THREE MAIN SUBUNITS: A, B AND C.  
CC -!- SUBCELLULAR LOCATION: MITOCHONDRIAL.  
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN  
CC (SPOT N153) IS: 5.5, ITS MW IS: 55 KD.  
CC -!- SIMILARITY: BELONGS TO THE ATPASE ALPHA/BETA CHAINS FAMILY.  
DR PROSITE: PS00152; ATPASE\_ALPHA\_BETA; PARTIAL.  
KW ATP synthesis; CF(1); Hydrogen ion transport;  
KW Hydrolyase; ATP-binding; Mitochondrion.  
FT NON\_TER 1 1  
FT NON\_TER 15 15  
SQ SEQUENCE 15 AA; 1629 MW; 3580CB725CCB8D9 CRC64;

Query Match 60.6%; Score 20; DB 1; Length 15;  
Best Local Similarity 60.0%; Pred. No. 1.2e+02;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QGILE 5  
||:|  
DB 7 QGVLD 11

RESULT 2  
HPAL\_RANES STANDARD; PRT; 13 AA.  
ID HPAL\_RANES  
AC P32415;  
DT 01-OCT-1993 (Rel. 27, Created)  
DT 01-OCT-1993 (Rel. 27, Last sequence update)  
DT 01-OCT-1993 (Rel. 27, Last annotation update)  
DE HEMOLYTIC PROTEIN A1 (FRAGMENT).  
OS Rana esculenta (Edible frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;  
OC Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Raninae; Rana.  
RN [1]  
RP SEQUENCE.  
RC TISSUE-SKIN SECRETION;  
RX MEDLINE; 90198965.  
RA Simmaco M., de Blase D., Severini C., Alta M., Erspamer G.F.,  
RA Barra D., Bossa F.;  
RT "Purification and characterization of bioactive peptides from skin  
RT extracts of Rana esculenta.";  
RL Biochim. Biophys. Acta 1033:318-323(1990).  
CC -!- FUNCTION: SHOWS HEMOLYTIC ACTIVITY.  
CC -!- SUBCELLULAR LOCATION: SECRETED.  
CC -!- TISSUE SPECIFICITY: SKIN.  
DR PIR: S09018; S09018.  
KW Amphibian skin; Amidation; Hemolysis.

FT MOD\_RES 13 13  
FT NON\_TER 13 13  
SQ SEQUENCE 13 AA; 1390 MW; C6BA768B9DFE587D CRC64;  
  
Query Match 48.5%; Score 16; DB 1; Length 13;  
Best Local Similarity 50.0%; Pred. No. 8.4e+02;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2 GILERV 7  
||:|  
DB 7 GILSQL 12

RESULT 3  
NUPM\_HUMAN  
ID NUPM\_HUMAN STANDARD; PRT; 13 AA.  
AC P51970;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE NADH-UBIQUINONE OXIDOREDUCTASE 19 KD SUBUNIT (EC 1.6.5.3)  
DE (EC 1.6.99.3) (COMPLEX I-19KD) (CI-19KD) (COMPLEX I-PGIV) (CI-PGIV)  
DE (FRAGMENT).  
GN NDUPA8.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.  
RN [1]  
RP SEQUENCE.  
RC TISSUE-KIDNEY;  
RX MEDLINE; 97295305.  
RA Sarto C., Marocchi A., Sanchez J.-C., Giannone B., Frutiger S.,  
RA Golaz O., Wilkins M.R., Doro G., Cappellano F., Hughes G.J.,  
RA Hochstrasser D.F., Mocarelli P.;  
RT "Renal cell carcinoma and normal kidney protein expression.";  
RL Electrophoresis 18:599-604(1997).  
CC -!- FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY  
CC CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED  
CC TO BE UBIQUINONE.  
CC -!- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.  
CC -!- SUBUNIT: COMPLEX I IS COMPOSED OF ABOUT 40 DIFFERENT SUBUNITS.  
CC THIS IS A COMPONENT OF THE HYDROPHOBIC FRACTION.  
CC -!- SUBCELLULAR LOCATION: MITOCHONDRIAL.  
CC -!- SIMILARITY: BELONGS TO THE COMPLEX I 19 KD SUBUNIT FAMILY.  
DR SWISS-2DPAGE; P51970; HUMAN.  
DR MIM: 603359; -.  
KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion.  
FT NON\_TER 13 13  
SQ SEQUENCE 13 AA; 1428 MW; 5A64EE91C92AF767 CRC64;

Query Match 48.5%; Score 16; DB 1; Length 13;  
Best Local Similarity 75.0%; Pred. No. 8.4e+02;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GILE 5  
||:|  
DB 2 GIVE 5

RESULT 4  
YGDH\_THEAC  
ID YGDH\_THEAC STANDARD; PRT; 14 AA.  
AC Q05213;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 01-JUN-1994 (Rel. 29, Last annotation update)  
DE HYPOTHETICAL PROTEIN IN GLUCOSE DEHYDROGENASE GENE 3'REGION  
DE (FRAGMENT).  
OS Thermoplasma acidophilum.  
OC Archaea; Euryarchaeota; Thermoplasmatales; Thermoplasmaceae;  
OC Thermoplasma.

RNA SEQUENCE FROM N.A.  
RC STRAIN-DSM 1728:  
RX MEDLINE; 93170285.  
RT Bright J.R., Byrom D., Danson M.J., Hough D.W., Towner P.;  
RT "Cloning, sequencing and expression of the gene encoding glucose  
RT dehydrogenase from the thermophilic archaeon Thermoplasma  
RT acidophilum";  
RL Eur. J. Biochem. 211:549-554(1993).  
CC -----  
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CC -----  
DR EMBL; X59788; CAA42451.1; -.  
DR PIR; S29789; S29789.  
KW Hypothetical protein.  
FT NON\_TER 14  
SQ SEQUENCE 14 AA; 1674 MW; 685A1FFF36529944 CRC64;

Query Match 45.5%; Score 15; DB 1; Length 14;  
Best Local Similarity 40.0%; Pred. No. 1.5e+03;  
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 ILERV 7  
Db 4 LLKRI 8

RESULT 5  
CDN2\_LITGI STANDARD; PRT; 15 AA.  
AC P56247;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 15-JUL-1998 (Rel. 36, Last annotation update)  
DE CAERIDIN 2.  
OS Litoria gilleni.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;  
OC Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae; Litoria.  
[1]  
RN SEQUENCE, AND MASS SPECTROMETRY.  
RC TISSUE-PAROTOID GLAND;  
RA Waugh R.J., Stone D.J.M., Bowie J.H., Wallace J.C., Tyler M.J.;  
RT "Peptides from Australian frogs. The structures of the caerins and  
RT caeridins from Litoria gilleni";  
RL J. Chem. Res. 139:937-961(1993).  
CC -1- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR  
CC ANTIBIOTIC ACTIVITY.  
CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN PAROTOID AND/OR ROSTRAL  
CC GLANDS.  
CC -1- MASS SPECTROMETRY: MW=1408; METHOD=FAB.  
KW Amphibian skin; Amidation.  
FT MOD\_RES 15  
SQ SEQUENCE 15 AA; 1410 MW; 06F1BBF272550CBF CRC64;

Query Match 45.5%; Score 15; DB 1; Length 15;  
Best Local Similarity 50.0%; Pred. No. 1.6e+03;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GILERV 7  
Db 1 GLLDV 6

RESULT 6  
TRP5\_LEUMA

ID TRP5\_LEUMA STANDARD; PRT; 10 AA.  
AC P81737;  
DT 15-FEB-2000 (Rel. 39, Created)  
DT 15-FEB-2000 (Rel. 39, Last sequence update)  
DT 15-FEB-2000 (Rel. 39, Last annotation update)  
DE TACHYKININ-RELATED PEPTIDE 5 (LEMTRP 5).  
OS Leucophaea maderae (Madeira cockroach).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;  
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;  
OC Blateroidea; Blaberidae; Leucophaea.  
[1]  
RN SEQUENCE.  
RP TISSUE-MIDGUT;  
RC MEDLINE; 97053012.  
RX Muren J.E., Naessel D.R.;  
RA "Isolation of five tachykinin-related peptides from the midgut of  
RT the cockroach Leucophaea maderae: existence of N-terminally extended  
RT isoforms";  
RL Regul. Pept. 65:185-196(1996).  
RN [2]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RC TISSUE-BRAIN;  
RX MEDLINE; 97269266.  
RA Muren J.E., Naessel D.R.;  
RT "Seven tachykinin-related peptides isolated from the brain of the  
RT Madeira cockroach; evidence for tissue-specific expression of  
RT isoforms";  
RL Peptides 18:7-15(1997).  
CC -1- FUNCTION: MYOACTIVE PEPTIDE. INCREASES THE AMPLITUDE AND FREQUENCY  
CC OF SPONTANEOUS CONTRACTIONS AND TONUS OF HINDGUT MUSCLE.  
CC -1- TISSUE SPECIFICITY: MIDGUT AND BRAIN.  
CC -1- MASS SPECTROMETRY: MW=1033.2; METHOD=WALDI-MS.  
CC -1- SIMILARITY: SOME SIMILARITY TO TACHYKININS.  
KW Tachykinin; Neuropeptide; Amidation.  
FT MOD\_RES 10  
SQ SEQUENCE 10 AA; 1033 MW; C452CD66D9C8769D CRC64;

Query Match 42.4%; Score 14; DB 1; Length 10;  
Best Local Similarity 66.7%; Pred. No. 1.8e+03;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QGI 3  
Db 7 QGV 9

RESULT 7  
BPPB\_AGKHA STANDARD; PRT; 11 AA.  
ID BPPB\_AGKHA  
AC P01021;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 15-JUL-1998 (Rel. 36, Last annotation update)  
DE BRADYKININ-POTENTIATING PEPTIDE B (ANGIOTENSIN-CONVERTING  
DE ENZYME INHIBITOR).  
OS Agkistrodon halys blomhoffii (Mamushi) (Gloydius blomhoffii).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Lepidosauria;  
OC Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae;  
OC Agkistrodon.  
[1]  
RN SEQUENCE.  
RP TISSUE-VENOM;  
RC Kato H., Suzuki T.;  
RA "Amino acid sequence of bradykinin-potentiating peptide isolated from  
RT the venom of Agkistrodon halys blomhoffii";  
RL Proc. Jpn. Acad. B, Phys. Biol. Sci. 46:176-181(1970).  
CC -1- FUNCTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE  
CC ANGIOTENSIN-CONVERTING ENZYME AND ENHANCES THE ACTION OF  
CC BRADYKININ BY INHIBITING THE KINASES THAT INACTIVATE IT.  
CC IT ACTS AS AN INDIRECT HYPOTENSIVE AGENT.  
DR PIR; A01254; XASNEA.  
KW Hypotensive agent; Venom.

FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
SQ SEQUENCE 11 AA; 1199 MW; 295CBF0627741777 CRC64;

Query Match 42.4%; Score 14; DB 1; Length 11;  
Best Local Similarity 50.0%; Pred. No. 2e+03;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QGILER 6  
Db 1 QGLPPR 6

RESULT 8  
CD11\_LITXA STANDARD; PRT; 12 AA.  
AC P56245; P81253;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE CAERIDIN 1.1/1.2/1.3.  
OS Litoria xanthomera (Orange-thighed frog), Litoria splendida,  
OS Litoria gilleni, and Litoria chloris (Blue-thighed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;  
OC Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae; Litoria.  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RC SPECIES=L.XANTHOMERA;  
RX MEDLINE; 97374000.  
RA Steinborner S.T., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.,  
RA Ramsay S.L.;  
RT "New caerin antibacterial peptides from the skin glands of the  
RT Australian tree frog Litoria xanthomera.";  
RL J. Pept. Sci. 3:181-185(1997).  
RN [2]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RC SPECIES=L.SPLENIDA; TISSUE=PAROTOID GLAND;  
RX Stone D.J.M., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.;  
RT "Peptides from Australian frogs. Structures of the caerins and  
RT caeridin 1 from Litoria splendida.";  
RL J. Chem. Soc. Perkin Trans. 1:3173-3178(1992).  
RN [3]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RC SPECIES=L.GILLEN; TISSUE=PAROTOID GLAND;  
RX Waugh R.J., Stone D.J.M., Bowie J.H., Wallace J.C., Tyler M.J.;  
RT "Peptides from Australian frogs. The structures of the caerins and  
RT caeridins from Litoria gilleni.";  
RL J. Chem. Res. 139:937-961(1993).  
RN [4]  
RP SEQUENCE, AND MASS SPECTROMETRY (CAERIDINS 1.1, 1.2 AND 1.3).  
RC SPECIES=L.GILLEN;  
RX Hu P., Gross M.L.;  
RT "Two isomeric alpha and beta aspartyl dodecapeptides and their  
RT cyclic amino succinyl analogue from the Australian tree frog  
RT Litoria gilleni.";  
RL Aust. J. Chem. 48:1981-1987(1995).  
RN [5]  
RP SEQUENCE.  
RC SPECIES=L.CHLORIS; TISSUE=SKIN;  
RX MEDLINE; 98175802.  
RA Steinborner S.T., Currie G.J., Bowie J.H., Wallace J.C., Tyler M.J.;  
RT "New antibiotic caerin 1 peptides from the skin secretion of the  
RT Australian tree frog Litoria chloris. Comparison of the activities of  
RT the caerin 1 peptides from the genus Litoria.";  
RL J. Pept. Res. 51:121-126(1998).  
CC -1- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR  
CC ANTIBIOTIC ACTIVITY.  
CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS IN L.  
CC XANTHOMERA OR SPECIFICALLY BY THE SKIN PAROTOID AND/OR ROSTRAL  
CC GLANDS IN L. SPLENDIDA AND L. GILLEN.  
CC -1- PTM: ISOMERIZATION ALPHA-BETA OF THE ASP-4 RESIDUE IN CAERIDIN  
CC 1.2; A CYCLIC SUCCINIMIDE MAY BE FORMED BETWEEN ASP-4 AND GLY-5

CC RESIDUES IN CAERIDIN 1.3.  
CC -1- MASS SPECTROMETRY: MM-1140; METHOD=FAB.  
CC -1- MISCELLANEOUS: THE RESULTS FOR MASS SPECTROMETRY OF CAERIDIN 1.1  
CC IS 1140 IN REF.1, REF.3 AND REF.4, WHILE IN REF.2 IT IS 1139.  
CC Amphibian skin; Amidation.  
FT MOD\_RES 12 12 AMIDATION  
SQ SEQUENCE 12 AA; 1141 MW; 2822551A33772728 CRC64;

Query Match 42.4%; Score 14; DB 1; Length 12;  
Best Local Similarity 50.0%; Pred. No. 2.2e+03;  
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GILE 5  
Db 1 GLLD 4

RESULT 9  
CD14\_LITXA STANDARD; PRT; 12 AA.  
AC P56246;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE CAERIDIN 1.4.  
OS Litoria xanthomera (Orange-thighed frog), and  
OS Litoria chloris (Blue-thighed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;  
OC Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae; Litoria.  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RC SPECIES=L.XANTHOMERA;  
RX MEDLINE; 97374000.  
RA Steinborner S.T., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.,  
RA Ramsay S.L.;  
RT "New caerin antibacterial peptides from the skin glands of the  
RT Australian tree frog Litoria xanthomera.";  
RL J. Pept. Sci. 3:181-185(1997).  
RN [2]  
RP SEQUENCE.  
RC SPECIES=L.CHLORIS; TISSUE=SKIN;  
RX MEDLINE; 98175802.  
RA Steinborner S.T., Currie G.J., Bowie J.H., Wallace J.C., Tyler M.J.;  
RT "New antibiotic caerin 1 peptides from the skin secretion of the  
RT Australian tree frog Litoria chloris. Comparison of the activities of  
RT the caerin 1 peptides from the genus Litoria.";  
RL J. Pept. Res. 51:121-126(1998).  
CC -1- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR  
CC ANTIBIOTIC ACTIVITY.  
CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.  
CC -1- MASS SPECTROMETRY: MM-1096; METHOD=FAB.  
CC Amphibian skin; Amidation.  
FT MOD\_RES 12 12 AMIDATION  
SQ SEQUENCE 12 AA; 1097 MW; 28225503E3772728 CRC64;

Query Match 42.4%; Score 14; DB 1; Length 12;  
Best Local Similarity 50.0%; Pred. No. 2.2e+03;  
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GILE 5  
Db 1 GLLD 4

RESULT 10  
CHEP\_PARID STANDARD; PRT; 13 AA.  
ID CHEP\_PARID  
AC P42718;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)



DE CHEMOTACTIC PEPTIDE.  
 OS Parapolybia indica.  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;  
 OC Vespoidea; Vespidae; Polistinae; Parapolybia.  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=VENOM;  
 RA Toki T., Yasuhara T., Nakajima T.;  
 RT "Isolation and sequential analysis of peptides on the venom sac of  
 RT Parapolybia indica."  
 RL Eisei Dobutsu 39:105-111(1988).  
 KW Chemotaxis; Amidation.  
 FT MOD\_RES 13 13  
 SQ SEQUENCE 13 AA; 1298 MW; 5C950CE8E39D5873 CRC64;

Query Match 42.4%; Score 14; DB 1; Length 13;

Best Local Similarity 33.3%; Pred. No. 2.4e+03;

Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 GILERV 7

Db 3 GLLKGI 8

RESULT 11

FIBB\_HYLLA

ID FIBB\_HYLLA STANDARD; PRT; 13 AA.

AC P14472;

DT 01-JAN-1990 (Rel. 13, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 01-FEB-1994 (Rel. 28, Last annotation update)

DE FIBRINOPEPTIDE B.

OS Hylobates lar (Common gibbon).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

OC Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.

RN [1]

RP SEQUENCE.

RX MEDLINE; 70294424.

RA Moss G.A., Doolittle R.F., Roberts B.F.;

RT "Gibbon fibrinopeptides: identification of a glycine-serine allelism

RT at position B-3."

RL Science 170:468-470(1970).

CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT

CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET

CC AGGREGATION.

CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS

CC (ALPHA, BETA, & GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.

CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY

CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA

CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES

CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.

DR PROSITE; PS00514; FIBRIN\_AG\_C\_DOMAIN; PARTIAL.

KW Blood coagulation; Plasma.

FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

FT VARIANT 11 11 S -> G.

FT NON\_TER 13 13

SQ SEQUENCE 13 AA; 1406 MW; 7D944D60187D698F CRC64;

Query Match

Best Local Similarity 42.4%; Score 14; DB 1; Length 13;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QGI 3

Db 1 QGV 3

RESULT 12

FIBB\_MANLE

ID FIBB\_MANLE STANDARD; PRT; 14 AA.

AC P14474;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 01-FEB-1994 (Rel. 28, Last annotation update)  
 DE FIBRINOPEPTIDE B.  
 OS Mandrillus leucophaeus (Drill) (Papio leucophaeus).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae;  
 OC Mandrillus.  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE; 691115139.  
 RA Doolittle R.F., Glasgow C., Moss G.A.;  
 RT "Characterization of fibrinopeptides A and B from a drill (Mandrillus  
 RT leucophaeus)."  
 RL Biochim. Biophys. Acta 175:217-219(1969).  
 CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT  
 CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET  
 CC AGGREGATION.  
 CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS  
 CC (ALPHA, BETA, & GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.  
 CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY  
 CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA  
 CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES  
 CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.  
 DR PROSITE; PS00514; FIBRIN\_AG\_C\_DOMAIN; PARTIAL.  
 KW Blood coagulation; Plasma.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT NON\_TER 14 14  
 SQ SEQUENCE 14 AA; 1434 MW; 6695B0F11EF72E1B CRC64;

Query Match

Best Local Similarity 42.4%; Score 14; DB 1; Length 14;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QGI 3

Db 1 QGV 3

RESULT 13

MY14\_EISFO

ID MY14\_EISFO STANDARD; PRT; 14 AA.

AC P46979;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DE MYOACTIVE TETRADECAPEPTIDE (ETP).

OS Eisenia foetida (Common branding worm) (Common dung-worm).

OC Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;

OC Lumbricina; Lumbricidae; Eisenia.

RN [1]

RP SEQUENCE, AND SYNTHESIS.

RC TISSUE=GUT;

RX MEDLINE; 96087879.

RA Ukenu K., Oumi T., Matsushima O., Ikeda T., Fujita T., Minakata H.,

RA Nomoto K.;

RT "A novel gut tetradecapeptide isolated from the earthworm, Eisenia

RT foetida."

RL Peptides 16:995-999(1995).

CC -1- FUNCTION: HAS A STIMULATIVE EFFECT ON THE CONTRACTION OF GUT

CC MUSCLES.

CC -1- SIMILARITY: TO INSECTS ALLATOTROPIN.

KW Neuropeptide; Amidation.

FT MOD\_RES 14 14

AMIDATION.

SQ SEQUENCE 14 AA; 1478 MW; CC9ABEF941CD91AD CRC64;

Query Match

Best Local Similarity 42.4%; Score 14; DB 1; Length 14;

Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```
QY 2 GILERV 7
| :|:
Db 5 GAADRI 10

RESULT 14
UN37_CLOPA
ID UN37_CLOPA STANDARD; PRT; 14 AA.
AC P81358;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE UNKNOWN PROTEIN CP 37 FROM 2D-PAGE (FRAGMENT).
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
OC Clostridium.
RN [1]
RP SEQUENCE.
RC STRAIN-W5;
RX MEDLINE; 98291870.
RA Flengsrud R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal
sequence analysis of proteins from Clostridium pasteurianum W5.";
RL Electrophoresis 19:802-806(1998).
CC -|- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
NON_TER 14
FT NON_TER 14
SQ SEQUENCE 14 AA; 1579 MW; 05384662DEF89210 CRC64;

Query Match 42.4%; Score 14; DB 1; Length 14;
Best Local Similarity 56.7%; Pred. No. 2.6e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QGI 3
| :|:
Db 10 QGV 12

RESULT 15
LPL_TETH
ID LPL_TETH STANDARD; PRT; 15 AA.
AC P21234;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-MAY-1991 (Rel. 18, Last annotation update)
DE LEU LEADER PEPTIDE.
OS Thermus aquaticus (subsp. thermophilus).
OC Bacteria; Thermus/Deinococcus group; Thermus group; Thermus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-HB8;
RX MEDLINE; 88121725.
RA Croft J.E., Love D.R., Bergquist P.L.;
RT "Expression of leucine genes from an extremely thermophilic bacterium
in Escherichia coli.";
RL Mol. Gen. Genet. 210:490-497(1987).
CC -|- FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS
OF LEUCINE.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X06604; CAA29823.1;
DR PIR; S00901; LFTWL.
KW Leader peptide; Leucine biosynthesis.
SQ SEQUENCE 15 AA; 1666 MW; C2F107A386D7620B CRC64;

Query Match 42.4%; Score 14; DB 1; Length 15;
Best Local Similarity 50.0%; Pred. No. 2.7e+03;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 ILER 6
| :|:
Db 8 VLDR 11

RESULT 16
MALT_BACTO
ID MALT_BACTO STANDARD; PRT; 15 AA.
AC P80072;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE MALTASE (EC 3.2.1.20) (ALPHA-GLUCOSIDASE I) (FRAGMENT).
OS Bacillus thermoamyloliquefaciens.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
RN [1]
RP SEQUENCE.
RC STRAIN-KP1071 / FERM P8477;
RX MEDLINE; 92209510.
RA Suzuki Y., Yonezawa K., Hattori M., Takii Y.;
RT "Assignment of Bacillus thermoamyloliquefaciens KP1071
alpha-glucosidase I to an exo-alpha-1,4-glucosidase, and its striking
similarity to bacillary oligo-1,6-glucosidases in N-terminal sequence
and in structural parameters calculated from the amino acid
composition.";
RL Eur. J. Biochem. 205:249-256(1992).
CC -|- CATALYTIC ACTIVITY: HYDROLYSIS OF TERMINAL, NON-REDUCING
1,4-LINKED D-GLUCOSE RESIDUES WITH RELEASE OF D-GLUCOSE.
CC -|- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
KNOWN AS THE ALPHA-AMYLASE FAMILY.
CC PIR; S21240; S21240.
DR Hydrolyase; Glycosidase.
KW NON_TER 15
FT NON_TER 15
SQ SEQUENCE 15 AA; 1929 MW; 62B4CE501F2D3042 CRC64;

Query Match 42.4%; Score 14; DB 1; Length 15;
Best Local Similarity 14.3%; Pred. No. 2.7e+03;
Matches 1; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 OGILERV 7
| :|:
Db 8 EGVYQI 14

RESULT 17
PA2B_VIPBO
ID PA2B_VIPBO STANDARD; PRT; 12 AA.
AC P31859;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE PHOSPHOLIPASE A2, BASIC (EC 3.1.1.4) (PHOSPHATIDYLCHOLINE
2-ACYLHYDROLASE) (FRAGMENT).
OS Vipera berus orientalis (Viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Lepidosauria;
OC Squamata; Scieroglossa; Serpentes; Colubroidea; Viperidae; Viperinae;
OC Vipera.
RN [1]
RP SEQUENCE.
RC TISSUP-VENOM;
RX MEDLINE; 74128698.
RA Delori P.J.;
RT "Purification and physicochemical, chemical and biological properties
of a toxic A2 phospholipase isolated from the venom of viperidae
snakes: Vipera berus.";
RL Biochimie 55:1031-1045(1973).
```

CC -!- FUNCTION: PA2 CATALYZES THE CALCIUM-DEPENDENT HYDROLYSIS OF THE  
 CC 2-ACYL GROUPS IN 3-SN-PHOSPHOGLYCERIDES.  
 CC -!- CATALYTIC ACTIVITY: PHOSPHATIDYLCHOLINE + H(2)O - 1-ACYLGLYCERYL-  
 CC PHOSPHOCHOLINE + A FATTY ACID ANION.  
 CC -!- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.  
 DR PROSITE; PS00118; PA2\_HIS; PARTIAL.  
 DR PROSITE; PS00119; PA2\_ASP; PARTIAL.  
 KW Hydrolase; Lipid degradation; Calcium; Venom.  
 FT NON\_TER 12 12  
 SQ SEQUENCE 12 AA; 1412 MW; D054351A89969879 CRC64;

Query Match 39.4%; Score 13; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ILE 5  
 |||  
 Db 9 ILE 11

RESULT 18  
 UP01\_CABEL  
 ID UP01\_CABEL STANDARD; PRT; 12 AA.  
 AC P59554;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE UNKNOWN PROTEIN FROM 2D-PAGE (SPOT 1) (FRAGMENT).  
 OS Caenorhabditis elegans.  
 CC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;  
 CC Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=BRISTOL N2;  
 RA MEDLINE; 97295299.  
 RX Bini L., Heid H., Liberatori S., Geier G., Pallini V., Zwilling R.;  
 RT "Two-dimensional gel electrophoresis of Caenorhabditis elegans  
 RT homogenates and identification of protein spots by microsequencing.";  
 RL Electrophoresis 18:557-562(1997).  
 FT NON\_TER 12 12  
 SQ SEQUENCE 12 AA; 1409 MW; 8DC4A7105316905A CRC64;

Query Match 39.4%; Score 13; DB 1; Length 12;  
 Best Local Similarity 50.0%; Pred. No. 3.7e+03;  
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 ILE 6  
 |||  
 Db 6 IMEX 9

RESULT 19  
 CBRL\_VESCR  
 ID CBRL\_VESCR STANDARD; PRT; 13 AA.  
 AC P01518;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE CRABROLIN.  
 OS Vespa crabro (European hornet).  
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 CC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;  
 CC Vespidae; Vespidae; Vespinae; Vespa.  
 RN [1]  
 RP SEQUENCE  
 RC TISSUE=VENOM;  
 RX MEDLINE; 84289390.  
 RA Argiolas A., Pisano J.J.;  
 RT "Isolation and characterization of two new peptides, mastoparan C and  
 RT crabrolin, from the venom of the European hornet, Vespa crabro.";  
 RL J. Biol. Chem. 259:10106-10111(1984).

RN [2]  
 RP SYNTHESIS, AND ANTIMICROBIAL ACTIVITY.  
 RX MEDLINE; 97419326.  
 RA Krishnakumari V., Nagaraj R.;  
 RT "Antimicrobial and hemolytic activities of crabrolin, a 13-residue  
 RT peptide from the venom of the European hornet, Vespa crabro, and its  
 RT analogs.";  
 RL J. Pept. Res. 50:88-93(1997).  
 CC -!- FUNCTION: MAST CELL DEGRANULATING PEPTIDE. INDUCES THE CHEMOTAXIS  
 CC OF NEUTROPHILS. HAS ANTIMICROBIAL AND HEMOLYTIC ACTIVITY.  
 DR PIR; A01781; JZVHP1.  
 KW Mast cell degranulation; Chemotaxis; Venom; Amidation; Antibiotic.  
 FT MOD\_RES 13 13  
 SQ SEQUENCE 13 AA; 1497 MW; 515EP8FCFA8D2407 CRC64;

Query Match 39.4%; Score 13; DB 1; Length 13;  
 Best Local Similarity 40.0%; Pred. No. 4e+03;  
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 ILE 7  
 || :  
 Db 5 ILRKI 9

RESULT 20  
 FARB\_ASCSU  
 ID FARB\_ASCSU STANDARD; PRT; 13 AA.  
 AC P43173;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-FEB-1996 (Rel. 33, Last annotation update)  
 DE FMRFAMIDE-LIKE NEUROPEPTIDE AFIL.  
 OS Ascaris suum (pig roundworm) (Ascaris lumbricoides).  
 CC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Ascaridida;  
 CC Ascaridoidea; Ascarididae; Ascaris.  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE; 95380362.  
 RA Cowden C., Stretton A.O.W.;  
 RT "Eight novel FMRFamide-like neuropeptides isolated from the nematode  
 RT Ascaris suum.";  
 RL Peptides 16:491-500(1995).  
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 13 13  
 SQ SEQUENCE 13 AA; 1495 MW; 9CAEC650D6886B05 CRC64;

Query Match 39.4%; Score 13; DB 1; Length 13;  
 Best Local Similarity 75.0%; Pred. No. 4e+03;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GILE 5  
 |||  
 Db 4 GISE 7

RESULT 21  
 HPB9\_RANES  
 ID HPB9\_RANES STANDARD; PRT; 13 AA.  
 AC P32416;  
 DT 01-OCT-1993 (Rel. 27, Created)  
 DT 01-OCT-1993 (Rel. 27, Last sequence update)  
 DT 01-OCT-1993 (Rel. 27, Last annotation update)  
 DE HEMOLYTIC PROTEIN B9 (FRAGMENT).  
 OS Rana esculenta (Edible frog).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;  
 CC Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.  
 RN [1]  
 RP SEQUENCE  
 RC TISSUE=SKIN SECRETION;

```

RX MEDLINE: 90198965.
RA Simmaco M., de Blase D., Severini C., Alta M., Erspaner G.F.,
RA Barra D., Bossa F.;
RT "Purification and characterization of bioactive peptides from skin
RT extracts of Rana esculenta.";
RL Blochm. Biophys. Acta 1033:318-323(1990).
CC -1- FUNCTION: SHOWS HEMOLYTIC ACTIVITY.
CC -1- SUBCELLULAR LOCATION: SECRETED.
CC -1- TISSUE SPECIFICITY: SKIN.
DR PIR: S09019; S09019.
KW Amphibian skin; Amidation; Hemolysis.
FT MOD_RES 13 13
FT NON_TER 13 13
SQ SEQUENCE 13 AA: 1402 MW: C6B41A765DF9287D CRC64;

Query Match 39.4%; Score 13; DB 1; Length 13;
Best Local Similarity 33.3%; Pred. No. 4e+03;
Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GILERV 7
Db 7 GLLGKL 12

RESULT 22
CRBL_VESOR 1511 MW: D86EDA955ABEFA12 CRC64;
ID CRBL_VESOR STANDARD; PRT; 14 AA.
AC P17236;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-AUG-1990 (Rel. 15, Last annotation update)
DE HISTAMINE RELEASING PEPTIDE II (HR-II).
OS Vespa orientalis (Oriental hornet).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Vespoidea; Vespidae; Vespinae; Vespa.
RN [1]
RP SEQUENCE.
RC TISSUE=VENOM;
RA Miroshnikov A. I., Snezhkova L.G., Nazimov I.V., Reshetova O.I.,
RA Rozynov B.V., Gushchin I.S.;
RT "Structure and properties of histamine releasing peptides from the
RT venom of Vespa orientalis hornet.";
RL Bioorg. Khim. 7:1467-1477(1981).
CC -1- FUNCTION: MAST CELL DEGRANULATING PEPTIDE. INDUCES THE CHEMOTAXIS
CC OF NEUTROPHILS.
DR PIR: JN0390; JN0390.
KW Mast cell degranulation; Chemotaxis; Venom; Amidation.
FT MOD_RES 14 14
FT NON_TER 14 14
SQ SEQUENCE 14 AA: 1524 MW: 22015B4A6CDEFD38 CRC64;

Query Match 39.4%; Score 13; DB 1; Length 14;
Best Local Similarity 50.0%; Pred. No. 4.3e+03;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 OGIL 4
Db 11 KGLL 14

RESULT 23
IF2G_RAT 1402 MW: C6B41A765DF9287D CRC64;
ID IF2G_RAT STANDARD; PRT; 14 AA.
AC P81795;
DT 15-FEB-2000 (Rel. 39, Created)
DT 15-FEB-2000 (Rel. 39, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE EUKARYOTIC TRANSLATION INITIATION FACTOR 2 GAMMA SUBUNIT (EIF-2-
DE GAMMA) (PP42) (FRAGMENT).
GN EIF2S3 OR EIF2G.
OS Rattus norvegicus (Rat).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE.
RC TISSUE=LIVER;
RA MEDLINE: 96374441.
RA Gil C., Plana M., Riera M., Itarte E.;
RT "Rat liver pp49, a protein that forms complexes with protein kinase
RT CK2, is composed of the beta and the gamma subunits of translation
RT initiation factor eIF-2.";
RL Biochem. Biophys. Res. Commun. 225:1052-1057(1996).
CC -1- FUNCTION: EIF-2 FUNCTIONS IN THE EARLY STEPS OF PROTEIN SYNTHESIS
CC BY FORMING A TERNARY COMPLEX WITH GTP AND INITIATOR TRNA. THIS
CC COMPLEX BINDS TO A 40S RIBOSOMAL SUBUNIT, FOLLOWED BY MRNA BINDING
CC TO FORM A 43S PREINITIATION COMPLEX. JUNCTION OF THE 60S RIBOSOMAL
CC SUBUNIT TO FORM THE 80S INITIATION COMPLEX IS PRECEDED BY
CC HYDROLYSIS OF THE GTP BOUND TO EIF-2 AND RELEASE OF AN EIF-2-GDP
CC BINARY COMPLEX. IN ORDER FOR EIF-2 TO RECYCLE AND CATALYZE ANOTHER
CC ROUND OF INITIATION, THE GDP BOUND TO EIF-2 MUST EXCHANGE WITH GTP
CC BY WAY OF A REACTION CATALYZED BY EIF-2B.
CC -1- SUBUNIT: HETEROTRIMER COMPOSED OF AN ALPHA, A BETA, AND A GAMMA
CC CHAIN.
CC -1- SIMILARITY: TO GTP-DEPENDENT ELONGATION FACTORS.
KW Initiation factor; Protein biosynthesis; GTP-binding.
FT NON_TER 1 1
FT NON_TER 14 14
SQ SEQUENCE 14 AA: 1511 MW: D86EDA955ABEFA12 CRC64;

Query Match 39.4%; Score 13; DB 1; Length 14;
Best Local Similarity 40.0%; Pred. No. 4.3e+03;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GILER 6
Db 10 GIVSK 14

RESULT 24
MY14_PHEVI 1402 MW: C6B41A765DF9287D CRC64;
ID MY14_PHEVI STANDARD; PRT; 14 AA.
AC P46980;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE MYOACTIVE TETRADECAPEPTIDE (PTP).
OS Pheretima vittata (Earthworm).
OC Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaeta;
OC Lumbriclna; Megascolecidae; Pheretima.
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=GUT;
RX MEDLINE: 96087879.
RA Ukena K., Oumi T., Matsushima O., Ikeda T., Fujita T., Minakata H.,
RA Nomoto K.;
RT "A novel gut tetradecapeptide isolated from the earthworm, Eisenia
RT foetida.";
RL Peptides 16:995-999(1995).
CC -1- FUNCTION: HAS A STIMULATIVE EFFECT ON THE CONTRACTION OF GUT
CC MUSCLES.
CC -1- SIMILARITY: TO INSECTS ALLATOTROPIN.
KW Neuropeptide; Amidation.
FT MOD_RES 14 14
FT NON_TER 14 14
SQ SEQUENCE 14 AA: 1522 MW: DA40BEE67CCD91AD CRC64;

Query Match 39.4%; Score 13; DB 1; Length 14;
Best Local Similarity 33.3%; Pred. No. 4.3e+03;
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GILERV 7
Db 5 GSADRI 10

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RESULT 25
ACPH_RABIT
ID ACPH_RABIT STANDARD; PRT; 6 AA.
AC P25154;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE ACYLAMINO-ACID-RELEASING ENZYME (EC 3.4.19.1) (ACYL-PEPTIDE HYDROLASE)
DE (APH) (ACYLAMINOACYL-PEPTIDASE) (FRAGMENT).
GN APEH.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Lagomorpha; Leporidae; Oryctolagus.
RN [1]
RP SEQUENCE.
RC TISSUE=MUSCLE;
RM MEDLINE; 92222120.
RX Krishna R.G., Chin C.C.O., Wold F.;
RT "N-terminal sequence analysis of N alpha-acetylated proteins after
RT unblocking with N-acylaminoacyl-peptide hydrolase.";
RL Anal. Biochem. 199;45:50(1991).
CC -1- FUNCTION: THIS ENZYME CATALYZES THE HYDROLYSIS OF THE AMINO-
CC TERMINAL PEPTIDE BOND OF AN N-ACETYLATED PEPTIDE TO GENERATE
CC AN N-ACETYLATED AA AND A PEPTIDE WITH A FREE AMINO-TERMINUS.
CC IT PREFERENTIALLY CLEAVES OFF AC-ALA, AC-MET AND AC-SER.
CC -1- CATALYTIC ACTIVITY: ACYLAMINOACYL-PEPTIDE + H(2)O = ACYLAMINO
CC ACID + PEPTIDE.
CC -1- SUBUNIT: HOMOTETRAMER.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S9C; ALSO KNOWN AS THE
CC PROLYL OLIGOPEPTIDASE FAMILY.
DR PROSITE; PS00708; PRO_ENDOPEP_SER; PARTIAL.
KW Hydrolase; Acetylation.
FT MOD_RES 1 1 ACETYLATION.
FT NON_TER 6 6
SQ SEQUENCE 6 AA; 775 MW; 6732D6C40B16F000 CRC64;

Query Match 36.4%; Score 12; DB 1; Length 6;
Best Local Similarity 66.7%; Pred. No. 8.4e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 LER 6
DB 1 MER 3

RESULT 26
CU30_LOCFI
ID CU30_LOCFI STANDARD; PRT; 10 AA.
AC P11735;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CUTICLE PROTEIN 30 (LM-30) (LM-ACP 30) (FRAGMENT).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;
OC Acridomorpha; Acridoidea; Acrididae; Oedipodinae; Locusta.
RN [1]
RP SEQUENCE.
RX MEDLINE; 86108304.
RA Hoejrup P., Andersen S.O., Roepstorff P.;
RT "Isolation, characterization, and N-terminal sequence studies of
RT cuticular proteins from the migratory locust, Locusta migratoria.";
RL Eur. J. Biochem. 154:153-159(1986).
CC -1- FUNCTION: COMPONENT OF THE CUTICLE OF MIGRATORY LOCUST WHICH
CC CONTAINS MORE THAN 100 DIFFERENT STRUCTURAL PROTEINS.
DR PIR; C24802; C24802.
KW Structural protein; Cuticle.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 969 MW; 4973E36B58772877 CRC64;

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Query Match 36.4%; Score 12; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 5.2e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GIL 4
DB 1 GLL 3

RESULT 27
TRP9_LEUMA
ID TRP9_LEUMA STANDARD; PRT; 10 AA.
AC P81741;
DT 15-FEB-2000 (Rel. 39, Created)
DT 15-FEB-2000 (Rel. 39, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE TACHYKININ-RELATED PEPTIDE 9 (LEMPRP 9).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blaberoidea; Blaberidae; Leucophaea.
RN [1]
RP SEQUENCE AND MASS SPECTROMETRY.
RC TISSUE=BRAIN;
RM MEDLINE; 97269266.
RX Muren J.E., Naessel D.R.;
RT "Seven tachykinin-related peptides isolated from the brain of the
RT madeira cockroach; evidence for tissue-specific expression of
RT isoforms.";
RL Peptides 18:7-15(1997).
CC -1- FUNCTION: MYOACTIVE PEPTIDE. INCREASES THE AMPLITUDE AND FREQUENCY
CC OF SPONTANEOUS CONTRACTIONS AND TONUS OF HINDGUT MUSCLE.
CC -1- TISSUE SPECIFICITY: BRAIN.
CC -1- MASS SPECTROMETRY: MW=1081.5; METHOD=WALDI-MS.
CC -1- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 10 10
SQ SEQUENCE 10 AA; 1081 MW; 9E469D6D9C87685 CRC64;

Query Match 36.4%; Score 12; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 5.2e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QGI 3
DB 7 QGM 9

RESULT 28
URAL_HUMAN
ID URAL_HUMAN STANDARD; PRT; 10 AA.
AC P32118;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE UNKNOWN PROTEIN FROM 2D-PAGE OF RED BLOOD CELLS (SPOT 1) (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE.
RC TISSUE=ERYTHROCYTE;
RM MEDLINE; 94147970.
RX Golaz O., Hughes G.J., Frutiger S., Paquet N., Bairoch A.,
RA Pasquali C., Sanchez J.-C., Tissot J.-D., Appel R.D., Walzer C.,
RA Balant L., Hochstrasser D.F.;
RT "Plasma and red blood cell protein maps: update 1993.";
RL Electrophoresis 14:1223-1231(1993).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.4, ITS MW IS: 23 KD.

```

DR SWISS-2DPAGE; P32118; HUMAN.  
FT NON\_TER 1  
SQ NON\_TER 10  
SQ SEQUENCE 10 AA; 977 MW; 723C65BIADD0587B CRC64;

Query Match 36.4%; Score 12; DB 1; Length 10;  
Best Local Similarity 66.7%; Pred. No. 5.2e+03;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 OGI 3  
Db 3 EGI 5

RESULT 29  
CH60\_DROME  
ID CH60\_DROME STANDARD; PRT; 11 AA.  
AC P33380;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE MITOCHONDRIAL MATRIX PROTEIN P1 (60 KD CHAPERONIN) (HEAT SHOCK PROTEIN 60) (HSP-60) (PROTEIN CPN60) (GROEL PROTEIN) (FRAGMENT).  
GN MMP-P1 OR HSP60.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
RN [1]  
RP SEQUENCE.  
RC STRAIN=VALLECAS; TISSUE=WING IMAGINAL DISK;  
RX MEDLINE; 93272852.  
RA Santaren J.F., van Damme J., Puype M., Vandekerckhove J., Garcia-Bellido A.  
RT "Identification of Drosophila wing imaginal disc proteins by two-dimensional gel analysis and microsequencing."  
RL Exp. Cell Res. 206:220-226(1993).  
CC -!- FUNCTION: IMPLICATED IN MITOCHONDRIAL PROTEIN IMPORT AND MACROMOLECULAR ASSEMBLY. MAY FACILITATE THE CORRECT FOLDING OF IMPORTED PROTEINS. MAY ALSO PREVENT MISFOLDING AND PROMOTE THE REFOLDING AND PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS CONDITIONS IN THE MITOCHONDRIAL MATRIX (BY SIMILARITY).  
CC -!- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX (BY SIMILARITY).  
CC -!- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.  
DR FLYBASE: FBgn0010375; Mmp-P1.  
DR PROSITE: PS00296; CHAPERONINS\_CPN60; PARTIAL.  
KW Chaperone; ATP-binding; Mitochondrion.  
FT NON\_TER 1  
FT NON\_TER 11  
SQ SEQUENCE 11 AA; 1243 MW; 78501A366365A6DB CRC64;

Query Match 36.4%; Score 12; DB 1; Length 11;  
Best Local Similarity 50.0%; Pred. No. 5.7e+03;  
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 3 ILER 6  
Db 2 IIEQ 5

RESULT 30  
CRBL\_ICASP  
ID CRBL\_ICASP STANDARD; PRT; 13 AA.  
AC P17237;  
DT 01-AUG-1990 (Rel. 15, Created)  
DT 01-AUG-1990 (Rel. 15, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE CHEMOTACTIC PEPTIDE (I-CP).  
OS Icaria sp. (Ropalididae wasp).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;  
OC Vespoidea; Vespidae; Polistinae; Icaria.  
RN [1]  
RP SEQUENCE.  
RC TISSUE=VENOM;  
RA Yasuhara T., Itokawa H., Suzuki N., Nakamura H., Nakajima T.;  
RL (in) Izumiya N. (eds.);  
RL Peptide chemistry 1984, pp.177-182, Protein Research Foundation, Osaka (1985).  
RL -!- FUNCTION: MAST CELL DEGRANULATING PEPTIDE. INDUCES THE CHEMOTAXIS OF NEUTROPHILS.  
KW Mast cell degranulation; Chemotaxis; Venom; Amidation.  
FT MOD\_RES 13  
FT MOD\_RES 13 AMIDATION.  
SQ SEQUENCE 13 AA; 1353 MW; 348DBC7AA30A3768 CRC64;

Query Match 36.4%; Score 12; DB 1; Length 13;  
Best Local Similarity 66.7%; Pred. No. 6.7e+03;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 2 GIL 4  
Db 10 GLL 12

Search completed: June 30, 2000, 19:03:16  
Job time: 15039 sec



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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 30, 2000, 16:18:45 ; Search time 53.11 Seconds  
(without alignments)  
9.138 Million cell updates/sec

Title: US-08-833-506c-120  
Perfect score: 33  
Sequence: 1 QGILERV 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 225878 seqs, 69334122 residues

Total number of hits satisfying chosen parameters: 1120

Minimum DB seq length: 0  
Maximum DB seq length: 15

Post-processing: Minimum Match 0%  
Listing first 100 summaries

Database :

SPTREMBL\_12:\*  
1: sp.archaea:\*  
2: sp.bacteria:\*  
3: sp.fungi:\*  
4: sp.human:\*  
5: sp.invertebrate:\*  
6: sp.mammal:\*  
7: sp.mhc:\*  
8: sp.organelle:\*  
9: sp.phage:\*  
10: sp.plant:\*  
11: sp.rodent:\*  
12: sp.virus:\*  
13: sp.vertebrate:\*  
14: sp.unclassified:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	57.6	11	2	Q44237
2	19	57.6	15	2	Q54325
3	17.5	53.0	14	12	O10234
4	17	51.5	13	2	P74844
5	17	51.5	13	4	Q16406
6	16	48.5	11	7	O77910
7	16	48.5	12	2	Q53183
8	16	48.5	13	4	Q16007
9	16	48.5	15	12	Q97090
10	15	45.5	10	2	Q9X3M2
11	15	45.5	10	13	O73594
12	15	45.5	11	2	Q9X9S6
13	15	45.5	11	7	O77911
14	15	45.5	13	2	Q9X3J6
15	15	45.5	13	2	Q9X3E1
16	15	45.5	13	3	P87031
17	15	45.5	15	10	O65177
18	15	45.5	15	12	Q97092
19	15	45.5	15	12	Q97094
20	14.5	43.9	14	12	O10226

21	14.5	43.9	14	12	O10227
22	14.5	43.9	14	12	O10228
23	14.5	43.9	14	12	O10229
24	14.5	43.9	14	12	O10230
25	14.5	43.9	14	12	O10232
26	14.5	43.9	14	12	O10233
27	14.5	43.9	14	12	O10235
28	14	42.4	8	6	Q28866
29	14	42.4	9	4	O15892
30	14	42.4	9	4	P78484
31	14	42.4	10	2	Q60192
32	14	42.4	10	2	Q60194
33	14	42.4	10	2	Q52837
34	14	42.4	10	12	O64971
35	14	42.4	12	2	Q46039
36	14	42.4	12	2	Q53358
37	14	42.4	13	2	Q55094
38	14	42.4	14	2	Q54861
39	14	42.4	14	4	Q14342
40	14	42.4	15	2	Q46013
41	14	42.4	15	8	O78794
42	14	42.4	15	12	Q79359
43	14	42.4	15	12	Q97098
44	13	39.4	8	2	Q9X3K1
45	13	39.4	9	6	O46574
46	13	39.4	10	12	Q88082
47	13	39.4	10	12	Q82625
48	13	39.4	11	4	Q15997
49	13	39.4	12	2	P97134
50	13	39.4	12	12	O10421
51	13	39.4	13	2	Q47601
52	13	39.4	13	2	Q9XBV0
53	13	39.4	13	11	Q54684
54	13	39.4	14	2	Q47599
55	13	39.4	14	6	Q9XSL4
56	13	39.4	14	8	P92076
57	13	39.4	14	12	O10231
58	13	39.4	15	2	O69173
59	13	39.4	15	2	O52640
60	12	36.4	8	2	Q51594
61	12	36.4	8	11	O64024
62	12	36.4	8	11	O64025
63	12	36.4	9	4	O95574
64	12	36.4	9	12	Q84333
65	12	36.4	10	5	Q25355
66	12	36.4	10	5	Q25356
67	12	36.4	11	7	O77871
68	12	36.4	11	7	O77872
69	12	36.4	11	7	O77873
70	12	36.4	11	12	Q83083
71	12	36.4	12	6	O46664
72	12	36.4	13	4	Q14804
73	12	36.4	14	2	Q47335
74	12	36.4	14	2	Q92B42
75	12	36.4	14	2	Q9X715
76	12	36.4	14	2	Q9WW79
77	12	36.4	14	5	Q26075
78	12	36.4	14	10	Q9XGM4
79	12	36.4	15	2	O52059
80	12	36.4	15	5	O97430
81	12	36.4	15	8	Q35921
82	12	36.4	15	12	Q85713
83	12	36.4	15	12	Q45889
84	11	33.3	8	2	O16468
85	11	33.3	8	7	Q29810
86	11	33.3	8	10	Q42507
87	11	33.3	8	11	Q63898
88	11	33.3	8	12	Q83977
89	11	33.3	9	12	O71069
90	11	33.3	9	12	O65545
91	11	33.3	9	12	O83622
92	11	33.3	9	12	Q85723
93	11	33.3	9	12	Q85723

94 11 33.3 10 8 Q35013 meloidogyne  
 95 11 33.3 10 8 Q9XMB4 aegilops sq  
 96 11 33.3 11 2 Q47604 escherichia  
 97 11 33.3 11 2 P71228 escherichia  
 98 11 33.3 11 4 Q16217 homo sapien  
 99 11 33.3 11 4 Q94785 homo sapien  
 100 11 33.3 11 11 Q62207 mus musculu

## ALIGNMENTS

RESULT 1  
 Q44237  
 ID Q44237 PRELIMINARY; PRT; 11 AA.  
 AC Q44237;  
 DT 01-NOV-1996 (TReMBLrel. 01, Created)  
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
 DT 01-NOV-1996 (TReMBLrel. 01, Last annotation update)  
 DE GLUTAMINE SYNTHETASE (FRAGMENT).  
 GN GLNA.  
 OS Anabaena sp.  
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-PC6 7120;  
 RA WARNER L.E., LIGON P.J., STAHEL A.W., CURTIS S.E.;  
 RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-PC6 7120;  
 RA SCAPPINO L.A.;  
 RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U21853; AAA65652.1; -.  
 FT NON\_TER 11  
 SQ SEQUENCE 11 AA; 1316 MW; 0427DF84 CRC32;

Query Match 57.6%; Score 19; DB 2; Length 11;  
 Best Local Similarity 42.9%; Pred. No. 4.6e+02;  
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QGILERV 7  
 | : | : | :  
 Db 5 QEVLRKI 11

RESULT 2  
 Q54325  
 ID Q54325 PRELIMINARY; PRT; 15 AA.  
 AC Q54325;  
 DT 01-NOV-1996 (TReMBLrel. 01, Created)  
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
 DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)  
 DE CHLORAMPHENICOL ACETYLTRANSFERASE (FRAGMENT).  
 GN CAT.  
 OS Staphylococcus intermedius.  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
 OC Bacillus/Staphylococcus group; Staphylococcus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-PCW6;  
 RX MEDLINE; 96379895.  
 RA LODDER G., SCHWARZ S., GREGORY P., DYKE K.;  
 RT "Tandem duplication in ermC translational attenuator of the macrolide-  
 RT lincosamide-streptogramin B resistance plasmid pSES6 from  
 RT Staphylococcus equorum.";  
 RL Antimicrob. Agents Chemother. 40:215-217(1996).  
 DR EMBL; X82666; CAA57981.1; -.  
 FT Transferase.  
 KW NON\_TER 1  
 SQ SEQUENCE 15 AA; 1931 MW; 996BDE4C CRC32;

Query Match 57.6%; Score 19; DB 2; Length 15;  
 Best Local Similarity 57.1%; Pred. No. 6.5e+02;  
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QGILERV 7  
 | : | : | :  
 Db 5 QDIHRV 11

RESULT 3  
 O10234  
 ID O10234 PRELIMINARY; PRT; 14 AA.  
 AC O10234;  
 DT 01-JUL-1997 (TReMBLrel. 04, Created)  
 DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)  
 DT 01-MAY-1999 (TReMBLrel. 10, Last annotation update)  
 DE ENVELOPE GLYCOPROTEIN (FRAGMENT).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroviridae; Lentivirus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 98216723.  
 RA SALVI R., GARBUGLIA A.R., DI CARO A., PULCIANI S., MONTELLA F.,  
 RA BENEDETTO A.;  
 RT "Grossly defective nef gene sequences in a human immunodeficiency  
 RT virus type 1-seropositive long-term nonprogressor.";  
 RL J. Virol. 72:3646-3657(1998).  
 DR EMBL; U89854; AAC26093.1; -.  
 DR PFAM; PF00517; GP41; 1.  
 KW Envelope protein.  
 FT NON\_TER 1  
 SQ SEQUENCE 14 AA; 1733 MW; CBF88541 CRC32;

Query Match 53.0%; Score 17.5; DB 12; Length 14;  
 Best Local Similarity 71.4%; Pred. No. 1.3e+03;  
 Matches 5; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Qy 1 QGILERV 7  
 | : | : | :  
 Db 7 QG-LERI 12

RESULT 4  
 P74844  
 ID P74844 PRELIMINARY; PRT; 13 AA.  
 AC P74844;  
 DT 01-FEB-1997 (TReMBLrel. 02, Created)  
 DT 01-FEB-1997 (TReMBLrel. 02, Last sequence update)  
 DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)  
 DE SIGMA FACTOR (FRAGMENT).  
 GN FLIA.  
 OS Salmonella typhimurium.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Salmonella.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-168-94;  
 RX MEDLINE; 97311993.  
 RA BURNENS A.P., STANLEY J., SACK R., HUNZIKER P., BRODARD I.,  
 RA NICOLET J.;  
 RT "The flagellin N-methylase gene fljB and an adjacent serovar-specific  
 RT IS200 element in Salmonella typhimurium.";  
 RL Microbiology 143:1539-1547(1997).  
 DR EMBL; Z67749; CAA91563.1; -.  
 FT NON\_TER 13  
 SQ SEQUENCE 13 AA; 1459 MW; 0D3A47E3 CRC32;

Query Match 51.5%; Score 17; DB 2; Length 13;  
 Best Local Similarity 16.7%; Pred. No. 1.6e+03;

Matches 1; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 QGILER 6

Db 8 EGVMDK 13

RESULT 5

Q16406 ID Q16406 PRELIMINARY; PRT; 13 AA.

AC Q16406;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DE 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)

DE GHRH-R PROTEIN (FRAGMENT).

GN GHRH-R.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

OC Eutheria; Primates; Catarrhini; Homnidae; Homo.

RN [1]

RP SEQUENCE FROM N.A.

RA HASHIMOTO K., KOGA M., MOTOMURA T., KASAYAMA S., KOUHARA H.,

RA ONISHI T., ARIITA N., HAYAKAWA T., SATO B., KISHIMOTO T.;

RT "Identification of alternatively spliced messenger ribonucleic acid

RT encoding truncated growth hormone-releasing hormone receptor in human

RT pituitary adenomas";

RL J. Clin. Endocrinol. Metab. 80:2933-2939(1995).

DR EMBL; S79912; AAD14318.1; -.

FT NON\_TER 1

SQ SEQUENCE 13 AA; 1612 MW; 085914B2 CRC32;

Query Match

Best Local Similarity 51.58; Score 17; DB 4; Length 13;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GILERV 7

Db 8 GYWERV 13

RESULT 6

Q77910 ID Q77910 PRELIMINARY; PRT; 11 AA.

AC Q77910;

DT 01-NOV-1998 (TrEMBLrel. 08, Created)

DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)

DE MHC CLASS II B LOCUS 3 (FRAGMENT).

OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;

OC Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;

OC Perciformes; Labroidae; Cichlidae; Oreochromis.

RN [1]

RP SEQUENCE FROM N.A.

RA MALAGA-TRILLO E., MCANDREW B., VINCEK V., ZALESKA-RUTCYNSKA Z.,

RA SUELTMANN H., FIGUEROA F., KLEIN J.;

RT "Linkage relationships and haplotype polymorphism among cichlid Mhc

RT class II B loci";

RL Genetics 149:1527-1547(1998).

DR EMBL; AF050021; AAC41360.1; -.

KW MHC.

FT NON\_TER 1

FT NON\_TER 11

SQ SEQUENCE 11 AA; 1344 MW; 2E9158C4 CRC32;

Query Match

Best Local Similarity 48.58; Score 16; DB 7; Length 11;

Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GILERV 7

Db 1 GFLEYI 6

RESULT 7

Q53183 ID Q53183 PRELIMINARY; PRT; 12 AA.

AC Q53183;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DE BETA-SUBUNIT OF NITRILE HYDRATASE (FRAGMENT).

OS Rhodococcus sp.

OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;

OC Actinomycetales; Corynebacterineae; Nocardiaceae; Rhodococcus.

RN [1]

RP SEQUENCE FROM N.A.

RA STRAIN-N-774;

RA MEDLINE; 95072315.

RA HASHIMOTO Y., NISHIYAMA M., HORINOCHI S., BEPPU T.;

RT "Nitrile hydratase gene from Rhodococcus sp. N-774 requirement for its

RT downstream region for efficient expression.";

RL Biosci. Biotechnol. Biochem. 58:1859-1865(1994).

DR EMBL; D30033; BAA06273.1; -.

DR HSP; P13449; IAHJ.

FT NON\_TER 1

SQ SEQUENCE 12 AA; 1323 MW; 666FD346 CRC32;

Query Match

Best Local Similarity 48.58; Score 16; DB 2; Length 12;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QGILE 5

Db 5 EGYLE 9

RESULT 8

Q16007 ID Q16007 PRELIMINARY; PRT; 13 AA.

AC Q16007;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DE LYSOSOMAL ACID BETA-GALACTOSIDASE (FRAGMENT).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

OC Eutheria; Primates; Catarrhini; Homnidae; Homo.

RN [1]

RP SEQUENCE FROM N.A.

RA MORREAU H., BONTEIN E., ZHOU X.Y., D'AZZO A.;

RT "Organization of the gene encoding human lysosomal beta-

RT galactosidase.";

RL DNA Cell Biol. 10:495-504(1991).

DR EMBL; S59584; AAB19814.1; -.

FT NON\_TER 13

SQ SEQUENCE 13 AA; 1482 MW; 615C03BB CRC32;

Query Match

Best Local Similarity 48.58; Score 16; DB 4; Length 13;

Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GILERV 7

Db 3 GFLVRI 8

RESULT 9

Q97090

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ID Q97090 PRELIMINARY; PRT; 15 AA.
AC Q97090:
DT 01-FEB-1997 (TREMBlrel. 02, Created)
DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE GAG POLYPROTEIN (FRAGMENT).
GN GAG.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LAI.
RX MEDLINE; 98184535.
RA WEI Q., FULTZ P.N.;
RT "Extensive diversification of human immunodeficiency virus type 1
RT subtype B strains during dual infection of a chimpanzee that
RT progressed to AIDS.";
RL J. Virol. 72:3005-3017(1998).
DR EMBL; U56889; AAC59299.1; -.
KW Polypeptide.
FT NON_TER 1
SQ SEQUENCE 15 AA; 1577 MW; 6B94DD64 CRC32;

Query Match 48.5%; Score 16; DB 12; Length 15;
Best Local Similarity 50.0%; Pred. No. 3e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 OGIL 6
DB 10 EGDLD 15

RESULT 10
Q9X3M2 PRELIMINARY; PRT; 10 AA.
ID Q9X3M2:
AC Q9X3M2:
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE CYTOCHROME B (FRAGMENT).
GN PETB.
OS Prochlorococcus sp.
OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
OC Prochlorococcus.
RN [1]
RP SEQUENCE FROM N.A.
RA URBACH E., CHISHOLM S.W.;
RT "Genetic diversity in Prochlorococcus populations flow cytometrically
RT sorted from the Sargasso Sea and Gulf Stream.";
RL Limnol. Oceanogr. 43:1615-1630(1998).
DR EMBL; AF070219; AAD23269.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1076 MW; BCB27A24 CRC32;

Query Match 45.5%; Score 15; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QGI 3
DB 5 QGI 7

RESULT 11
Q73594 PRELIMINARY; PRT; 10 AA.
ID Q73594:
AC Q73594:
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE ZAX-2 (FRAGMENT).

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OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WHITE LEHORN; TISSUE=WHOLE EMBRYOS;
RX MEDLINE; 98141813.
RA PEALE F.V., MASON K., HUNTER A.W., BOTHWELL M.;
RT "Multiplex display polymerase chain reaction amplifies and resolves
RT related sequences sharing a single moderately conserved domain.";
RL Anal. Biochem. 256:158-168(1998).
DR EMBL; U34617; AAC36455.1; -.
FT NON_TER 1
FT NON_TER 10
SQ SEQUENCE 10 AA; 1068 MW; 381E8670 CRC32;

Query Match 45.5%; Score 15; DB 13; Length 10;
Best Local Similarity 50.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GILERV 7
DB 5 GLPKRV 10

RESULT 12
Q9X9S6 PRELIMINARY; PRT; 11 AA.
ID Q9X9S6:
AC Q9X9S6:
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE HYPOTHETICAL 1.2 KD PROTEIN (FRAGMENT).
GN ORE9.
OS Streptomyces lividans.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TK21.
RX MEDLINE; 99328982.
RA MARTINEZ-COSTA O.H., MARTIN-TRIANA A.J., MARTINEZ E.,
RA FERNANDEZ-MORENO M.A., MALPARTIDA F.;
RT "An additional regulatory gene for actinorhodin production in
RT Streptomyces lividans involves a LysR-type transcriptional
RT regulator.";
RL J. Bacteriol. 181:4353-4364(1999).
DR EMBL; Y18818; CAB51138.1; -.
KW Hypothetical protein.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 11 AA; 1160 MW; C64AD8BF CRC32;

Query Match 45.5%; Score 15; DB 2; Length 11;
Best Local Similarity 42.9%; Pred. No. 3.7e+03;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 OGILERV 7
DB 2 QGVRAHV 8

RESULT 13
Q77911 PRELIMINARY; PRT; 11 AA.
ID Q77911:
AC Q77911:
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE MHC CLASS II B LOCUS 3 (FRAGMENT).
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;

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OC Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;  
 OC Perciformes; Labroidae; Cichlidae; Oreochromis.  
 RN [1]  
 RX MEDLINE; 98315113.  
 RA MALAGA-TRILLO E., MCANDREW B., VINCEK V., ZALESKA-RUTCZYNSKA Z.,  
 RA SUELTSMANN H., FIGUEROA F., KLEIN J.;  
 RT "Linkage relationships and haplotype polymorphism among cichlid Mhc  
 RT class II B loci."  
 RL Genetics 149:1527-1547(1998).  
 DR EMBL; AF050022; AAC41361.1; -.  
 KW MHC.  
 FT NON\_TER 1 1  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1401 MW; FF3CDF9 CRC32;

Query Match 45.5%; Score 15; DB 7; Length 11;  
 Best Local Similarity 75.0%; Pred. No. 3.7e+03;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GILE 5  
 Db 1 GFLE 4

RESULT 14  
 O9X3J6 PRELIMINARY; PRT; 13 AA.  
 AC O9X3J6;  
 DT 01-NOV-1999 (TREMBLrel. 12, Created)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)  
 DE CYTOCHROME B (FRAGMENT).  
 GN PETB.  
 OS Prochlorococcus sp.  
 OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;  
 OC Prochlorococcus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA URBACH E., CHISHOLM S.W.;  
 RT "Genetic diversity in Prochlorococcus populations flow cytometrically  
 RT sorted from the Sargasso Sea and Gulf Stream."  
 RL Limnol. Oceanogr. 43:1615-1630(1998).  
 DR EMBL; AF070189; RAD23225.1; -.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 13 AA; 1473 MW; ECD3C1B2 CRC32;

Query Match 45.5%; Score 15; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 4.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QGI 3  
 Db 7 QGI 9

RESULT 15  
 O9X3E1 PRELIMINARY; PRT; 13 AA.  
 AC O9X3E1;  
 DT 01-NOV-1999 (TREMBLrel. 12, Created)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)  
 DE CYTOCHROME B (FRAGMENT).  
 GN PETB.  
 OS Prochlorococcus sp.  
 OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;  
 OC Prochlorococcus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA URBACH E., CHISHOLM S.W.;

RT "Genetic diversity in Prochlorococcus populations flow cytometrically  
 RT sorted from the Sargasso Sea and Gulf Stream."  
 RL Limnol. Oceanogr. 43:1615-1630(1998).  
 DR EMBL; AF070141; RAD20755.1; -.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 13 AA; 1434 MW; 14865A9B CRC32;

Query Match 45.5%; Score 15; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 4.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QGI 3  
 Db 7 QGI 9

RESULT 16  
 P87031 PRELIMINARY; PRT; 13 AA.  
 AC P87031;  
 DT 01-JUL-1997 (TREMBLrel. 04, Created)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)  
 DE ORF YGR126W (FRAGMENT).  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;  
 OC Saccharomycetaceae; Saccharomycetes.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA VAN DYCK L., SKALA J., DE WERGIFOSSE P., PURNELLE B., TALLA E.,  
 RA NAWROCKI A., DEL BINO S., GOFFEAU A.;  
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA MIPS;  
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; 272912; CAA97139.2; -.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 13 AA; 1594 MW; AC1F58C5 CRC32;

Query Match 45.5%; Score 15; DB 3; Length 13;  
 Best Local Similarity 28.6%; Pred. No. 4.4e+03;  
 Matches 2; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 QGILERV 7  
 Db 5 KGFFHRI 11

RESULT 17  
 O65177 PRELIMINARY; PRT; 15 AA.  
 AC O65177;  
 DT 01-AUG-1998 (TREMBLrel. 07, Created)  
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)  
 DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)  
 DE TURGOR RESPONSIVE PROTEIN HOMOLOG (FRAGMENT).  
 OS Mesembryanthemum crystallinum (Common ice plant).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;  
 OC core eudicots; Caryophyllales; Alzooceae;  
 OC Mesembryanthemum.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-ROOT;  
 RA MICHALOWSKI C.B., BOHNERT H.J.;  
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF054444; AAC14178.1; -.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 15 AA; 1607 MW; AD52368C CRC32;



Db 7 QG-LER 11

## RESULT 22

O10228 PRELIMINARY; PRT; 14 AA.  
 ID O10228  
 AC O10228;  
 DT 01-JUL-1997 (Tremblrel. 04, Created)  
 DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)  
 DT 01-MAY-1999 (Tremblrel. 10, Last annotation update)  
 DE ENVELOPE GLYCOPROTEIN (FRAGMENT).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 98216723.  
 RA SALVI R., GARBUGLIA A.R., DI CARO A., PULCIANI S., MONTELLA F.,  
 RA BENEDETTO A.;  
 RT "Grossly defective nef gene sequences in a human immunodeficiency  
 virus type 1-seropositive long-term nonprogressor.";  
 RL J. Virol. 72:3646-3657(1998).  
 DR EMBL; U89848; AAC26087.1; -.  
 DR PFAM; PF00517; GP41; 1.  
 KW Envelope protein.  
 FT NON\_TER 1  
 SQ SEQUENCE 14 AA; 1691 MW; C5EBD4F9 CRC32;

Query Match 43.9%; Score 14.5; DB 12; Length 14;  
 Best Local Similarity 83.3%; Pred. No. 6.1e+03;  
 Matches 5; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 QGILER 6

Db 7 QG-LER 11

## RESULT 23

O10229 PRELIMINARY; PRT; 14 AA.  
 ID O10229  
 AC O10229;  
 DT 01-JUL-1997 (Tremblrel. 04, Created)  
 DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)  
 DT 01-MAY-1999 (Tremblrel. 10, Last annotation update)  
 DE ENVELOPE GLYCOPROTEIN (FRAGMENT).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 98216723.  
 RA SALVI R., GARBUGLIA A.R., DI CARO A., PULCIANI S., MONTELLA F.,  
 RA BENEDETTO A.;  
 RT "Grossly defective nef gene sequences in a human immunodeficiency  
 virus type 1-seropositive long-term nonprogressor.";  
 RL J. Virol. 72:3646-3657(1998).  
 DR EMBL; U89849; AAC26088.1; -.  
 DR PFAM; PF00517; GP41; 1.  
 KW Envelope protein.  
 FT NON\_TER 1  
 SQ SEQUENCE 14 AA; 1721 MW; DF06B562 CRC32;

Query Match 43.9%; Score 14.5; DB 12; Length 14;  
 Best Local Similarity 83.3%; Pred. No. 6.1e+03;  
 Matches 5; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 QGILER 6

Db 7 QG-LER 11

## RESULT 24

O10230 PRELIMINARY; PRT; 14 AA.  
 ID O10230  
 AC O10230;  
 DT 01-JUL-1997 (Tremblrel. 04, Created)  
 DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)  
 DT 01-MAY-1999 (Tremblrel. 10, Last annotation update)  
 DE ENVELOPE GLYCOPROTEIN (FRAGMENT).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 98216723.  
 RA SALVI R., GARBUGLIA A.R., DI CARO A., PULCIANI S., MONTELLA F.,  
 RA BENEDETTO A.;  
 RT "Grossly defective nef gene sequences in a human immunodeficiency  
 virus type 1-seropositive long-term nonprogressor.";  
 RL J. Virol. 72:3646-3657(1998).  
 DR EMBL; U89850; AAC26089.1; -.  
 DR PFAM; PF00517; GP41; 1.  
 KW Envelope protein.  
 FT NON\_TER 1  
 SQ SEQUENCE 14 AA; 1721 MW; DF06B562 CRC32;

Query Match 43.9%; Score 14.5; DB 12; Length 14;  
 Best Local Similarity 83.3%; Pred. No. 6.1e+03;  
 Matches 5; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 QGILER 6

Db 7 QG-LER 11

## RESULT 25

O10232 PRELIMINARY; PRT; 14 AA.  
 ID O10232  
 AC O10232;  
 DT 01-JUL-1997 (Tremblrel. 04, Created)  
 DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)  
 DT 01-MAY-1999 (Tremblrel. 10, Last annotation update)  
 DE ENVELOPE GLYCOPROTEIN (FRAGMENT).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 98216723.  
 RA SALVI R., GARBUGLIA A.R., DI CARO A., PULCIANI S., MONTELLA F.,  
 RA BENEDETTO A.;  
 RT "Grossly defective nef gene sequences in a human immunodeficiency  
 virus type 1-seropositive long-term nonprogressor.";  
 RL J. Virol. 72:3646-3657(1998).  
 DR EMBL; U89852; AAC26091.1; -.  
 DR PFAM; PF00517; GP41; 1.  
 KW Envelope protein.  
 FT NON\_TER 1  
 SQ SEQUENCE 14 AA; 1691 MW; C5EBD4F9 CRC32;

Query Match 43.9%; Score 14.5; DB 12; Length 14;  
 Best Local Similarity 83.3%; Pred. No. 6.1e+03;  
 Matches 5; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 QGILER 6

Db 7 QG-LER 11

## RESULT 26

O10233

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ID O10233 PRELIMINARY; PRT; 14 AA.
AC O10233;
DT 01-JUL-1997 (TRENBLrel. 04, Created)
DE 01-JUL-1997 (TRENBLrel. 04, Last sequence update)
DT 01-MAY-1999 (TRENBLrel. 10, Last annotation update)
DE ENVELOPE GLYCOPROTEIN (FRAGMENT).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 98216723.
RA SALVI R., GARBUGLIA A.R., DI CARO A., PULCIANI S., MONTELLA F.,
RA BENEDETTO A.;
RT "Grossly defective nef gene sequences in a human immunodeficiency
RT virus type 1-seropositive long-term nonprogressor.";
RL J. Virol. 72:3646-3657(1998).
DR EMBL: U89853; AAC26092.1; -.
DR PFAM: PF00517; GP41; 1.
KW Envelope protein.
FT NON_TER 1
SQ SEQUENCE 14 AA; 1691 MW; C5EBD4F9 CRC32;

Query Match 43.9%; Score 14.5; DB 12; Length 14;
Best Local Similarity 83.3%; Pred. No. 6.1e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 QGILER 6
DB 7 QG-LER 11

RESULT 27
O10235 PRELIMINARY; PRT; 14 AA.
ID O10235
AC O10235;
DT 01-JUL-1997 (TRENBLrel. 04, Created)
DT 01-JUL-1997 (TRENBLrel. 04, Last sequence update)
DT 01-MAY-1999 (TRENBLrel. 10, Last annotation update)
DE ENVELOPE GLYCOPROTEIN (FRAGMENT).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 98216723.
RA SALVI R., GARBUGLIA A.R., DI CARO A., PULCIANI S., MONTELLA F.,
RA BENEDETTO A.;
RT "Grossly defective nef gene sequences in a human immunodeficiency
RT virus type 1-seropositive long-term nonprogressor.";
RL J. Virol. 72:3646-3657(1998).
DR EMBL: U89855; AAC26094.1; -.
DR PFAM: PF00517; GP41; 1.
KW Envelope protein.
FT NON_TER 1
SQ SEQUENCE 14 AA; 1721 MW; DF06B562 CRC32;

Query Match 43.9%; Score 14.5; DB 12; Length 14;
Best Local Similarity 83.3%; Pred. No. 6.1e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 QGILER 6
DB 7 QG-LER 11

RESULT 28
Q28866 PRELIMINARY; PRT; 8 AA.
ID Q28866
AC Q28866;
DT 01-NOV-1996 (TRENBLrel. 01, Created)

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DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-MAY-1999 (TRENBLrel. 10, Last annotation update)
DE ACTIN PROTEIN (FRAGMENT).
GN ACTIN.
OS Megaptera novaeangliae (Humpback whale).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Cetacea; Mysticeti; Balaeopteridae;
OC Megaptera.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 94285813.
RA PALUMBI S.R., BAKER C.S.;
RT "Contrasting population structure from nuclear intron sequences and
RT mtDNA of humpback whales.";
RL Mol. Biol. Evol. 11:426-435(1994).
DR EMBL: S73467; AAD14118.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 906 MW; 4D7C9EF6 CRC32;

Query Match 42.4%; Score 14; DB 6; Length 8;
Best Local Similarity 66.7%; Pred. No. 2.3e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QGI 3
DB 6 QGV 8

RESULT 29
Q15892 PRELIMINARY; PRT; 9 AA.
ID Q15892
AC Q15892;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-AUG-1998 (TRENBLrel. 07, Last annotation update)
DE (CLONE XP3B4) (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homnidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=PLACENTA;
RA LEE C.C., YAZDANI A., WEHNERT M., BAILEY J., COUCH L., XIONG M.,
RA COOLBAUGH M.I., CHINAULT C.A., BALDINI A., LINDSAY E.A., ZHAO Z.Y.,
RA CASKEY C.T.H.;
RL Hum. Mol. Genet. 0:0-0(0).
DR EMBL: L32071; AAA73882.1; -.
FT NON_TER 1
FT NON_TER 9
SQ SEQUENCE 9 AA; 971 MW; A5838DF1 CRC32;

Query Match 42.4%; Score 14; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LER 6
DB 2 LER 4

RESULT 30
P78484 PRELIMINARY; PRT; 9 AA.
ID P78484
AC P78484;
DT 01-MAY-1997 (TRENBLrel. 03, Created)
DT 01-MAY-1997 (TRENBLrel. 03, Last sequence update)
DT 01-NOV-1998 (TRENBLrel. 08, Last annotation update)
DE FYN ONCOGENE, 3' END, CLONE PFYN-C-11. (FRAGMENT).
GN FYN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

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OC Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 RN [1]  
 RP SEQUENCE OF 90-98 FROM N.A.  
 RX MEDLINE; 88234523.  
 RA KAWAKAMI T., KAWAKAMI Y., AARONSON S.A., ROBBINS K.C.;  
 RT "Acquisition of transforming properties by FYN, a normal SRC-related  
 human gene."  
 RL Proc. Natl. Acad. Sci. U.S.A. 85:3870-3874(1988).  
 DR EMBL; M20284; AAA52491.1; -.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 9 AA; 1143 MW; C710793C CRC32;

Query Match 42.4%; Score 14; DB 4; Length 9;  
 Best Local Similarity 60.0%; Pred. No. 2.3e+05;  
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QGILE 5  
 | |  
 Db 4 QSFLE 8

Search completed: June 30, 2000, 16:18:47  
 Job time: 7898 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: June 30, 2000, 13:12:33 ; Search time 40.56 Seconds  
(without alignments)  
4.088 Million cell updates/sec

Title: US-08-833-506c-89  
Perfect score: 35  
Sequence: 1 VTQDDLQ 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 188963 seqs, 23686106 residues

Total number of hits satisfying chosen parameters: 76368

Minimum DB seq length: 0  
Maximum DB seq length: 15

Post-processing: Minimum Match 0%  
Listing first 100 summaries

Database : A\_Geneseq\_36:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	100.0	9	1 W81229	Human INOS peptide
2	35	100.0	9	1 W81294	Human INOS peptide
3	35	100.0	9	1 W81264	Human INOS peptide
4	35	100.0	12	1 W81228	Human INOS peptide
5	35	100.0	12	1 W81293	Human INOS peptide
6	35	100.0	12	1 W81268	Human INOS peptide
7	35	100.0	15	1 W81227	Human INOS peptide
8	35	100.0	15	1 W81292	Human INOS peptide
9	35	100.0	15	1 W81267	Human INOS peptide
10	31	88.6	15	1 W81223	Human INOS peptide
11	31	88.6	15	1 W81288	Human INOS peptide
12	30	85.7	10	1 W81265	Human INOS peptide
13	30	85.7	10	1 W81270	Human INOS peptide
14	26	74.3	9	1 W81266	Human INOS peptide
15	23	65.7	15	1 R20282	Beta-2 integrin pe
16	23	65.7	15	1 W02070	Human beta2 integr
17	22	62.9	8	1 W53913	Interleukin-1 rece
18	22	62.9	12	1 W35486	Proteoglycan-assoc
19	22	62.9	13	1 W35498	Pal A peptide from
20	22	62.9	14	1 W12358	Human hsp60 peptid
21	22	62.9	14	1 W33050	Human heat shock p
22	21	60.0	6	1 R29290	Nerve growth stimu
23	21	60.0	6	1 W05563	Ependymin peptide
24	21	60.0	9	1 W97963	Human synaptosomal
25	21	60.0	10	1 W97904	Human synaptosomal
26	21	60.0	11	1 R25221	Residues 150-160 o
27	21	60.0	14	1 R88681	Allergen Alt a 45
28	21	60.0	14	1 W30922	Birch pollen aller
29	20	57.1	6	1 W81217	Human INOS peptide
30	20	57.1	6	1 W81230	Human INOS peptide
31	20	57.1	6	1 W81295	Human INOS peptide
32	20	57.1	6	1 W81283	Human INOS peptide
33	20	57.1	6	1 W81269	Human INOS peptide
34	20	57.1	9	1 W81216	Human INOS peptide

35	20	57.1	9	1 W81282	Human INOS peptide
36	20	57.1	9	1 W97374	HA-1 R-allele sequ
37	20	57.1	9	1 W99197	Minor histocompati
38	20	57.1	10	1 R98521	Hepatitis C virus
39	20	57.1	12	1 W07166	Synthetic Nerve gr
40	20	57.1	12	1 W81281	Human INOS peptide
41	20	57.1	12	1 W81215	Human INOS peptide
42	20	57.1	13	1 W90086	Porcine G-protein
43	20	57.1	13	1 W99198	Porcine G-protein
44	20	57.1	13	1 W97414	Human INOS peptide
45	20	57.1	15	1 W90087	Porcine G-protein
46	20	57.1	15	1 W81280	Human INOS peptide
47	20	57.1	15	1 W81214	Human INOS peptide
48	19	54.3	8	1 R36141	Hepatitis C virus
49	19	54.3	8	1 R36142	Hepatitis C virus
50	19	54.3	9	1 R49202	HLA-A1 MAGE 1 ant
51	19	54.3	9	1 R51605	Mimotope nonapepti
52	19	54.3	9	1 R69980	Nonameric mimotope
53	19	54.3	9	1 R98728	Peptide 11 from 24
54	19	54.3	9	1 W10402	Antiphospholipid a
55	19	54.3	9	1 W67124	Antibody ACA-6501
56	19	54.3	9	1 W97375	HA-1 H-allele sequ
57	19	54.3	9	1 W99196	Minor histocompati
58	19	54.3	10	1 R49203	HLA-A3 MAGE 1 anti
59	19	54.3	10	1 R49203	HLA-A3 MAGE 1 anti
60	19	54.3	10	1 R65124	MAGE 1 immunogenic
61	19	54.3	11	1 R34189	Bacterial ribonucle
62	19	54.3	11	1 R42894	GPF - IE product,
63	19	54.3	11	1 W29200	Soluble I-As alpha
64	19	54.3	11	1 W29192	Soluble I-Ad alpha
65	19	54.3	11	1 W38430	Human dendritic ce
66	19	54.3	12	1 W17519	Aspergillus niger
67	19	54.3	13	1 P90435	Cyclophilin. Cyclo
68	19	54.3	13	1 W99199	vr cell KIAA0223 p
69	19	54.3	13	1 W97415	KIAA0223 polymorph
70	19	54.3	14	1 P90437	Cyclophilin. Cyclo
71	19	54.3	14	1 R25840	Peptide inhibitor
72	19	54.3	14	1 R67639	Epitope of Non-A N
73	19	54.3	14	1 R71655	Circumsporozoite a
74	19	54.3	14	1 W59112	FMDV non-structura
75	19	54.3	14	1 W71853	Mouse membrane typ
76	19	54.3	14	1 W78328	Random encoded pe
77	18	51.4	6	1 W54210	Human TSP43/Cvc-5
78	18	51.4	7	1 R61754	Human TSP43/Cvc-5
79	18	51.4	8	1 R73220	MBP peptide 79, po
80	18	51.4	8	1 R88694	Human TSH receptor
81	18	51.4	8	1 R95061	Allergen Alt a 12
82	18	51.4	8	1 R49204	Multidomain protei
83	18	51.4	9	1 R61863	HLA-A1 MAGE 1 anti
84	18	51.4	9	1 R61705	MBP peptide 79, po
85	18	51.4	9	1 W51031	HLA-A2.1 algorithm
86	18	51.4	9	1 W97572	Human fibrinogen g
87	18	51.4	9	1 W99195	T-cell epitope fro
88	18	51.4	10	1 R42377	Minor histocompati
89	18	51.4	10	1 R67279	C-myc proto-oncoge
90	18	51.4	10	1 R78486	Epitope recognised
91	18	51.4	10	1 R78383	Synthetic HRLV pep
92	18	51.4	10	1 W00813	Antigenic epitope
93	18	51.4	10	1 W03846	Myc epitope tag. O
94	18	51.4	10	1 W00684	Myc epitope. Const
95	18	51.4	10	1 W28854	Peptide comprising
96	18	51.4	10	1 W28626	hTLV-2 derived pep
97	18	51.4	10	1 W26631	Signalling inosito
98	18	51.4	10	1 W16450	Human MBP peptide
99	18	51.4	10	1 W16451	Human MBP peptide
100	18	51.4	10	1 W27324	Myc epitope tag. D

ALIGNMENTS

RESULT 1  
W81229

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ID W81229 standard; peptide; 9 AA.
AC W81229;
DE 30-APR-1999 (first entry)
KW Human iNOS peptide fragment PS-5267.
KW Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;
KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;
KW myocardial infarction; tissue rejection; transplantation; psoriasis;
KW autoimmune disease; multiple sclerosis.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Modified_site 9 /note= "Gln residue amidated"
FT W09845710-A1.
PD 15-OCT-1998.
PF 11-APR-1997; U06500.
PR 07-APR-1997; US-667777.
PA (WEBB/) WEBBER R.
PI Webber R.
DR WPI; 98-594495/50.
DE Detection of human inducible nitric oxide synthase - using an
PT immunoassay in which a sample is contacted with a specific binding
PT entity reactive with human iNOS or mimics.
PS Example 4; Page 36; 93pp; English.
CC This invention describes an immunoassay method where a sample with a
CC specific binding entity (e.g. a monoclonal antibody) reactive to human
CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used
CC to detect the presence of human iNOS protein in the sample. The method
CC can be used for the detection and quantitation of human iNOS in cells and
CC tissues for various pathophysiological conditions such as sepsis, septic
CC shock, myocardial infarction, rejection of tissue in organs following
CC transplantation, monitoring "flare ups" in certain autoimmune diseases
CC such as lupus, psoriasis, and multiple sclerosis. This sequence
CC represents a peptide from human iNOS which is used in the method of the
CC invention. 9 AA;
SQ Sequence 9 AA;

Query Match 100.0%; Score 35; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.5e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VTQDDLQ 7
DB 3 VTQDDLQ 9

RESULT 3
ID W81264 standard; peptide; 9 AA.
AC W81264;
DE 30-APR-1999 (first entry)
KW Human iNOS peptide fragment PS-5215.
KW Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;
KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;
KW myocardial infarction; tissue rejection; transplantation; psoriasis;
KW autoimmune disease; multiple sclerosis.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Modified_site 9 /note= "Gln residue amidated"
FT W09845710-A1.
PD 15-OCT-1998.
PF 11-APR-1997; U06500.
PR 07-APR-1997; US-667777.
PA (WEBB/) WEBBER R.
PI Webber R.
DR WPI; 98-594495/50.
DE Detection of human inducible nitric oxide synthase - using an
PT immunoassay in which a sample is contacted with a specific binding
PT entity reactive with human iNOS or mimics.
PS Example 12; Page 53; 93pp; English.
CC This invention describes an immunoassay method where a sample with a
CC specific binding entity (e.g. a monoclonal antibody) reactive to human
CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used
CC to detect the presence of human iNOS protein in the sample. The method
CC can be used for the detection and quantitation of human iNOS in cells and
CC tissues for various pathophysiological conditions such as sepsis, septic
CC shock, myocardial infarction, rejection of tissue in organs following
CC transplantation, monitoring "flare ups" in certain autoimmune diseases
CC such as lupus, psoriasis, and multiple sclerosis. This sequence
CC represents a peptide from human iNOS which is used in the method of the
CC invention. 9 AA;
SQ Sequence 9 AA;

Query Match 100.0%; Score 35; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.5e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VTQDDLQ 7
DB 3 VTQDDLQ 9

RESULT 4
ID W81228 standard; peptide; 12 AA.
AC W81228;
DE 30-APR-1999 (first entry)
KW Human iNOS peptide fragment PS-5266.
KW Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;

```

KW monoclonal antibody; mimic: quantitation; sepsis; septic shock; lupus;  
KW myocardial infarction; tissue rejection; transplantation; psoriasis;  
KW autoimmune disease; multiple sclerosis.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT Modified\_site 12 /note= "Asn residue amidated"  
PD WO9845710-A1.  
PF 15-OCT-1998.  
PR 11-APR-1997; U06500.  
PA (WEBB/) WEBBER R.  
PI Webber R;  
DR WPI: 98-594495/50.  
PT Detection of human inducible nitric oxide synthase - using an  
PT immunoassay in which a sample is contacted with a specific binding  
PT entity reactive with human iNOS or mimics.  
PS Example 4; Page 36; 93pp; English.  
CC This invention describes an immunoassay method where a sample with a  
CC specific binding entity (e.g. a monoclonal antibody) reactive to human  
CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used  
CC to detect the presence of human iNOS protein in the sample. The method  
CC can be used for the detection and quantitation of human iNOS in cells and  
CC tissues for various pathological conditions such as sepsis, septic  
CC shock, myocardial infarction, rejection of tissue in organs following  
CC transplantation, monitoring "flare ups" in certain autoimmune diseases  
CC such as lupus, psoriasis, and multiple sclerosis. This sequence  
CC represents a peptide from human iNOS which is used in the method of the  
CC invention.  
SQ Sequence 12 AA;

Query Match 100.0%; Score 35; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0.1;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VTQDDDLQ 7  
Db 3 VTQDDDLQ 9

## RESULT 5

W81293  
ID W81293 standard; peptide; 12 AA.  
AC W81293;  
DT 30-APR-1999 (first entry)  
DE Human iNOS peptide fragment for epitope mapping #14.  
KW Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;  
KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;  
KW myocardial infarction; tissue rejection; transplantation; psoriasis;  
KW autoimmune disease; multiple sclerosis; epitope mapping.  
OS Homo sapiens.  
PN WO9845710-A1.  
PD 15-OCT-1998.  
PF 11-APR-1997; U06500.  
PR 07-APR-1997; US-667777.  
PA (WEBB/) WEBBER R.  
PI Webber R;  
DR WPI: 98-594495/50.  
PT Detection of human inducible nitric oxide synthase - using an  
PT immunoassay in which a sample is contacted with a specific binding  
PT entity reactive with human iNOS or mimics.  
PS Example 4; Fig 7B; 93pp; English.  
CC This invention describes an immunoassay method where a sample with a  
CC specific binding entity (e.g. a monoclonal antibody) reactive to human  
CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used  
CC to detect the presence of human iNOS protein in the sample. The method  
CC can be used for the detection and quantitation of human iNOS in cells and  
CC tissues for various pathological conditions such as sepsis, septic  
CC shock, myocardial infarction, rejection of tissue in organs following  
CC transplantation, monitoring "flare ups" in certain autoimmune diseases  
CC such as lupus, psoriasis, and multiple sclerosis. This sequence  
CC represents a peptide from human iNOS which is used in the method of the

CC invention.  
SQ Sequence 12 AA;

Query Match 100.0%; Score 35; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0.1;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VTQDDDLQ 7  
Db 3 VTQDDDLQ 9

## RESULT 6

W81268  
ID W81268 standard; peptide; 12 AA.  
AC W81268;  
DT 30-APR-1999 (first entry)  
DE Human iNOS peptide fragment PS-5266.  
KW Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;  
KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;  
KW myocardial infarction; tissue rejection; transplantation; psoriasis;  
KW autoimmune disease; multiple sclerosis.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT Modified\_site 15 /note= "Lys residue amidated"

PN WO9845710-A1.

PD 15-OCT-1998.

PF 11-APR-1997; U06500.

PR 07-APR-1997; US-667777.

PA (WEBB/) WEBBER R.

PI Webber R;

DR WPI: 98-594495/50.

PT Detection of human inducible nitric oxide synthase - using an

PT immunoassay in which a sample is contacted with a specific binding

PT entity reactive with human iNOS or mimics.

PS Example 12; Page 54; 93pp; English.

CC This invention describes an immunoassay method where a sample with a  
CC specific binding entity (e.g. a monoclonal antibody) reactive to human  
CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used  
CC to detect the presence of human iNOS protein in the sample. The method  
CC can be used for the detection and quantitation of human iNOS in cells and  
CC tissues for various pathological conditions such as sepsis, septic  
CC shock, myocardial infarction, rejection of tissue in organs following  
CC transplantation, monitoring "flare ups" in certain autoimmune diseases  
CC such as lupus, psoriasis, and multiple sclerosis. This sequence  
CC represents a peptide from human iNOS which is used in the method of the  
CC invention.  
SQ Sequence 12 AA;

Query Match 100.0%; Score 35; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0.1;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VTQDDDLQ 7  
Db 3 VTQDDDLQ 9

## RESULT 7

W81227  
ID W81227 standard; peptide; 15 AA.  
AC W81227;  
DT 30-APR-1999 (first entry)  
DE Human iNOS peptide fragment PS-5265.  
KW Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;  
KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;  
KW myocardial infarction; tissue rejection; transplantation; psoriasis;  
KW autoimmune disease; multiple sclerosis.  
OS Homo sapiens.  
FH Key Location/Qualifiers

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FT Modified_site 15 /note= "Lys residue amidated"
PN WO9845710-A1.
PD 15-OCT-1998.
PF 11-APR-1997; U06500.
PR 07-APR-1997; US-66777.
PA (WEBB/) WEBBER R.
PI Webber R.
DR WPI: 98-594495/50.
PT Detection of human inducible nitric oxide synthase - using an
PT immunosay in which a sample is contacted with a specific binding
PT entity reactive with human iNOS or mimics.
PS Example 4; Page 36; 93pp; English.
CC This invention describes an immunoassay method where a sample with a
CC specific binding entity (e.g. a monoclonal antibody) reactive to human
CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used
CC to detect the presence of human iNOS protein in the sample. The method
CC can be used for the detection and quantitation of human iNOS in cells and
CC tissues for various pathophysiological conditions such as sepsis, septic
CC shock, myocardial infarction, rejection of tissue in organs following
CC transplantation, monitoring "flare ups" in certain autoimmune diseases
CC such as lupus, psoriasis, and multiple sclerosis. This sequence
CC represents a peptide from human iNOS which is used in the method of the
CC invention. 15 AA;
SQ Sequence 15 AA;

Query Match 100.0%; Score 35; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VTQDDLQ 7
DB 3 VTQDDLQ 9

RESULT 8
WO1292
ID W81292 standard; peptide; 15 AA.
AC W81292;
DT 30-APR-1999 (first entry)
DE Human iNOS peptide fragment for epitope mapping #13.
KW Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;
KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;
KW myocardial infarction; tissue rejection; transplantation; psoriasis;
KW autoimmune disease; multiple sclerosis; epitope mapping.
OS Homo sapiens.
PN WO9845710-A1.
PD 15-OCT-1998.
PF 11-APR-1997; U06500.
PR 07-APR-1997; US-66777.
PA (WEBB/) WEBBER R.
PI Webber R.
DR WPI: 98-594495/50.
PT Detection of human inducible nitric oxide synthase - using an
PT immunosay in which a sample is contacted with a specific binding
PT entity reactive with human iNOS or mimics.
PS Example 4; Fig 7B; 93pp; English.
CC This invention describes an immunoassay method where a sample with a
CC specific binding entity (e.g. a monoclonal antibody) reactive to human
CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used
CC to detect the presence of human iNOS protein in the sample. The method
CC can be used for the detection and quantitation of human iNOS in cells and
CC tissues for various pathophysiological conditions such as sepsis, septic
CC shock, myocardial infarction, rejection of tissue in organs following
CC transplantation, monitoring "flare ups" in certain autoimmune diseases
CC such as lupus, psoriasis, and multiple sclerosis. This sequence
CC represents a peptide from human iNOS which is used in the method of the
CC invention. 15 AA;
SQ Sequence 15 AA;

Query Match 100.0%; Score 35; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VTQDDLQ 7
DB 3 VTQDDLQ 9

RESULT 10
WO1223
ID W81223 standard; peptide; 15 AA.
AC W81223;
DT 30-APR-1999 (first entry)
DE Human iNOS peptide fragment PS-5261.
KW Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;
KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;
KW myocardial infarction; tissue rejection; transplantation; psoriasis;
KW autoimmune disease; multiple sclerosis.
OS Homo sapiens.
PN WO9845710-A1.
PD 15-OCT-1998.
PF 11-APR-1997; U06500.

Query Match 100.0%; Score 35; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VTQDDLQ 7
DB 3 VTQDDLQ 9

RESULT 9
WO1267
ID W81267 standard; peptide; 15 AA.
AC W81267;
DT 30-APR-1999 (first entry)
DE Human iNOS peptide fragment PS-5265.
KW Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;
KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;
KW myocardial infarction; tissue rejection; transplantation; psoriasis;
KW autoimmune disease; multiple sclerosis.
OS Homo sapiens.
PN WO9845710-A1.
PD 15-OCT-1998.
PF 11-APR-1997; U06500.
PR 07-APR-1997; US-66777.
PA (WEBB/) WEBBER R.
PI Webber R.
DR WPI: 98-594495/50.
PT Detection of human inducible nitric oxide synthase - using an
PT immunosay in which a sample is contacted with a specific binding
PT entity reactive with human iNOS or mimics.
PS Example 12; Page 54; 93pp; English.
CC This invention describes an immunoassay method where a sample with a
CC specific binding entity (e.g. a monoclonal antibody) reactive to human
CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used
CC to detect the presence of human iNOS protein in the sample. The method
CC can be used for the detection and quantitation of human iNOS in cells and
CC tissues for various pathophysiological conditions such as sepsis, septic
CC shock, myocardial infarction, rejection of tissue in organs following
CC transplantation, monitoring "flare ups" in certain autoimmune diseases
CC such as lupus, psoriasis, and multiple sclerosis. This sequence
CC represents a peptide from human iNOS which is used in the method of the
CC invention. 15 AA;
SQ Sequence 15 AA;

Query Match 100.0%; Score 35; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VTQDDLQ 7
DB 3 VTQDDLQ 9

RESULT 15
WO1267
ID W81267 standard; peptide; 15 AA.
AC W81267;
DT 30-APR-1999 (first entry)
DE Human iNOS peptide fragment PS-5265.
KW Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;
KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;
KW myocardial infarction; tissue rejection; transplantation; psoriasis;
KW autoimmune disease; multiple sclerosis.
OS Homo sapiens.
PN WO9845710-A1.
PD 15-OCT-1998.
PF 11-APR-1997; U06500.

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PR 07-APR-1997; US-667777.  
PA (WEBB/) WEBBER R.  
DR WPI: 98-594495/50.  
PT Detection of human inducible nitric oxide synthase - using an  
PT immunoassay in which a sample is contacted with a specific binding  
PT entity reactive with human iNOS or mimics.  
PS Example 4; Page 35; 93pp; English.  
CC This invention describes an immunoassay method where a sample with a  
CC specific binding entity (e.g. a monoclonal antibody) reactive to human  
CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used  
CC to detect the presence of human iNOS protein in the sample. The method  
CC can be used for the detection and quantitation of human iNOS in cells and  
CC tissues for various pathological conditions such as sepsis, septic  
CC shock, myocardial infarction, rejection of tissue in organs following  
CC transplantation, monitoring "flare ups" in certain autoimmune diseases  
CC such as lupus, psoriasis, and multiple sclerosis. This sequence  
CC represents a peptide from human iNOS which is used in the method of the  
SQ invention. 15 AA;

Query Match 88.6%; Score 31; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.89;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TQDDLQ 7  
Db 1 TQDDLQ 6

RESULT 11  
W81288  
ID W81288 standard; peptide; 15 AA.  
AC W81288; (first entry)  
DE Human iNOS peptide fragment for epitope mapping #9.  
DE Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;  
KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;  
KW myocardial infarction; tissue rejection; transplantation; psoriasis;  
KW autoimmune disease; multiple sclerosis; epitope mapping.  
OS Homo sapiens.  
PN W09845710-A1.  
PD 15-OCT-1998.  
PF 11-APR-1997; U06500.  
PR 07-APR-1997; US-667777.  
PA (WEBB/) WEBBER R.  
PI Webber R;  
DR WPI: 98-594495/50.  
PT Detection of human inducible nitric oxide synthase - using an  
PT immunoassay in which a sample is contacted with a specific binding  
PT entity reactive with human iNOS or mimics.  
PS Example 4; Fig 7A; 93pp; English.  
CC This invention describes an immunoassay method where a sample with a  
CC specific binding entity (e.g. a monoclonal antibody) reactive to human  
CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used  
CC to detect the presence of human iNOS protein in the sample. The method  
CC can be used for the detection and quantitation of human iNOS in cells and  
CC tissues for various pathological conditions such as sepsis, septic  
CC shock, myocardial infarction, rejection of tissue in organs following  
CC transplantation, monitoring "flare ups" in certain autoimmune diseases  
CC such as lupus, psoriasis, and multiple sclerosis. This sequence  
CC represents a peptide from human iNOS which is used in the method of the  
SQ invention. 15 AA;

Query Match 88.6%; Score 31; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.89;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TQDDLQ 7  
Db 1 TQDDLQ 6

Db 1 TQDDLQ 6  
RESULT 12  
W81265  
ID W81265 standard; peptide; 9 AA.  
AC W81265; (first entry)  
DE Human iNOS peptide fragment PS-5236.  
DE Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;  
KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;  
KW myocardial infarction; tissue rejection; transplantation; psoriasis;  
KW autoimmune disease; multiple sclerosis.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT Modified\_site 9 /note= "Leu residue amidated"  
PN W09845710-A1.  
PD 15-OCT-1998.  
PF 11-APR-1997; U06500.  
PR 07-APR-1997; US-667777.  
PA (WEBB/) WEBBER R.  
PI Webber R;  
DR WPI: 98-594495/50.  
PT Detection of human inducible nitric oxide synthase - using an  
PT immunoassay in which a sample is contacted with a specific binding  
PT entity reactive with human iNOS or mimics.  
PS Example 12; Page 53; 93pp; English.  
CC This invention describes an immunoassay method where a sample with a  
CC specific binding entity (e.g. a monoclonal antibody) reactive to human  
CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used  
CC to detect the presence of human iNOS protein in the sample. The method  
CC can be used for the detection and quantitation of human iNOS in cells and  
CC tissues for various pathological conditions such as sepsis, septic  
CC shock, myocardial infarction, rejection of tissue in organs following  
CC transplantation, monitoring "flare ups" in certain autoimmune diseases  
CC such as lupus, psoriasis, and multiple sclerosis. This sequence  
CC represents a peptide from human iNOS which is used in the method of the  
SQ invention. 9 AA;

Query Match 85.7%; Score 30; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.5e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VTQDDL 6  
Db 4 VTQDDL 9

RESULT 13  
W81270  
ID W81270 standard; peptide; 10 AA.  
AC W81270; (first entry)  
DE Human iNOS peptide fragment PS-5269.  
DE Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;  
KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;  
KW myocardial infarction; tissue rejection; transplantation; psoriasis;  
KW autoimmune disease; multiple sclerosis.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT Modified\_site 10 /note= "Leu residue amidated"  
PN W09845710-A1.  
PD 15-OCT-1998.  
PF 11-APR-1997; U06500.  
PR 07-APR-1997; US-667777.  
PA (WEBB/) WEBBER R.  
PI Webber R;  
DR WPI: 98-594495/50.  
PT Detection of human inducible nitric oxide synthase - using an

PT immunoassay in which a sample is contacted with a specific binding  
PT entity reactive with human iNOS or mimics.  
PS Example 12; Page 54; 93pp; English.  
CC This invention describes an immunoassay method where a sample with a  
CC specific binding entity (e.g. a monoclonal antibody) reactive to human  
CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used  
CC to detect the presence of human iNOS protein in the sample. The method  
CC can be used for the detection and quantitation of human iNOS in cells and  
CC tissues for various pathological conditions such as sepsis, septic  
CC shock, myocardial infarction, rejection of tissue in organs following  
CC transplantation, monitoring "flare ups" in certain autoimmune diseases  
CC such as lupus, psoriasis, and multiple sclerosis. This sequence  
CC represents a peptide from human iNOS which is used in the method of the  
CC invention.  
SQ Sequence 10 AA;

Query Match 85.7%; Score 30; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.91;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VTQDDL 6  
| | | | |  
DB 5 VTQDDL 10

RESULT 14  
W81266 ID W81266 standard; peptide; 9 AA.  
AC W81266;  
DE 30-APR-1999 (first entry)  
DE Human iNOS peptide fragment PS-5257.  
KW Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;  
KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;  
KW myocardial infarction; tissue rejection; transplantation; psoriasis;  
KW autoimmune disease; multiple sclerosis.  
OS Homo sapiens.  
FH Key Location/Qualifiers

FT Modified\_site 9 /note= "Asp residue amidated"  
FT W09845710-A1.

PD 15-OCT-1998.  
PD 11-APR-1997; U06500.  
PR 07-APR-1997; US-66777.  
PA (WEBB/) WEBBER R.  
PI Webber R;  
DR WPI; 98-594495/50.  
PT Detection of human inducible nitric oxide synthase - using an  
PT immunoassay in which a sample is contacted with a specific binding  
PT entity reactive with human iNOS or mimics.  
PS Example 12; Page 53; 93pp; English.  
CC This invention describes an immunoassay method where a sample with a  
CC specific binding entity (e.g. a monoclonal antibody) reactive to human  
CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used  
CC to detect the presence of human iNOS protein in the sample. The method  
CC can be used for the detection and quantitation of human iNOS in cells and  
CC tissues for various pathological conditions such as sepsis, septic  
CC shock, myocardial infarction, rejection of tissue in organs following  
CC transplantation, monitoring "flare ups" in certain autoimmune diseases  
CC such as lupus, psoriasis, and multiple sclerosis. This sequence  
CC represents a peptide from human iNOS which is used in the method of the  
CC invention.  
SQ Sequence 9 AA;

Query Match 74.3%; Score 26; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.5e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VTQDD 5  
| | | | |  
DB 5 VTQDD 9

RESULT 15  
R20282 ID R20282 standard; peptide; 15 AA.  
AC R20282;  
DE 10-APR-1992 (first entry)  
DE Beta-2 integrin peptide derived from CD11b alpha subunit.  
KW Immune response; phagocyte-mediated tissue damage; A domain; MAM;  
KW inflammation; CD11/CD18 complex; alpha subunit; CR3; M01; Mav-1;  
KW complement receptor type 3; heterodimer; collagen binding.  
OS Synthetic.  
PN W09119511-A.  
PD 26-DEC-1991.  
PF 18-JUN-1991; U04338.  
PR 18-JUN-1990; US-539842.  
PR 04-JAN-1991; US-637830.  
PA (GEHO-) GEN HOSPITAL CORP.  
PI Arnaout MA;  
DR WPI; 92-024197/03.  
PT Beta-2 integrin peptide CD11b, recombinant hetero-dimer  
PT CD11b/CD18 - or MAB against them; useful for inhibiting CD11/CD18  
PT mediated immune response in control of phagocyte-mediated tissue  
PT damage  
PS Claim 8; Page 73; 84pp; English.  
CC The peptide (SEQ ID NO: 29) corresponds to residues 750-764 of CD11b  
CC alpha subunit of beta 2 integrin. The peptide may be synthesised or  
CC prep'd. by recombinant techniques using the gene, the sequence of  
CC which was disclosed by Arnaout et al., J. Cell Biol. 106:2153 (1988).  
CC (References are also provided for the DNA sequences of human CD18,  
CC CD11c and CD11a). The peptide is capable of inhibiting a CD11/CD18  
CC mediated immune response and is useful for treatment of ischaemia  
CC reperfusion injury, burns, frostbite, acute arthritis, asthma and  
CC adult respiratory distress syndrome. It may also be used to block  
CC intra-islet infiltration of macrophages associated with insulin-  
CC dependent diabetes mellitus, and for controlling phagocyte-media-  
CC ted tissue damage to heart muscle during acute cardiac insuffi-  
CC ciency.  
CC See also R20256-R20299.  
SQ Sequence 15 AA;

Query Match 65.7%; Score 23; DB 1; Length 15;  
Best Local Similarity 86.7%; Pred. No. 43;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VTQDDL 6  
| | | | |  
DB 10 ICQDDL 15

RESULT 16  
W02070 ID W02070 standard; peptide; 15 AA.  
AC W02070;  
DE 09-APR-1997 (first entry)  
DE Human beta2 integrin subunit CD11b, residues 750-764.  
KW Beta2 integrin; A-domain; metal binding domain; inflammatory response;  
KW immune response; inhibition; phagocyte-mediated tissue injury;  
KW inflammation.  
OS Homo sapiens.  
PN W09624063-A1.  
PD 08-AUG-1996.  
PF 30-JAN-1996; U01314.  
PR 30-JAN-1995; US-380167.  
PA (GEHO ) GEN HOSPITAL CORP.  
PI Arnaout MA;  
DR WPI; 96-371576/37.

PT In vitro identification of integrin function antagonists - by  
PT measuring binding of A-domain peptide derived from integrin to  
PT ligand in presence and absence of candidate antagonist  
PS Disclosure; Page 11; 11pp; English.  
CC The sequences given in W02037-80 represent peptides derived from  
CC beta2 integrin, esp. A-domain and the metal binding domains. These



CC peptides were selected using the method of the invention which  
 CC screens compounds for their ability to inhibit the binding of a  
 CC selected integrin to a ligand which naturally binds to it. The  
 CC method comprises measuring the binding of an A-domain peptide  
 CC derived from the selected integrin, to the ligand in the presence  
 CC and absence of the test compound and determining whether the binding  
 CC is decreased. Identified compounds are capable of interfering with  
 CC certain cellular immune/inflammatory responses, particularly  
 CC phagocyte-mediated tissue injury and inflammation. The numbering  
 CC of the amino acid residues is based on the the deduced amino acid  
 CC sequence of the open reading frame of human CD11b from Arnaout et al.,  
 J. Cell. Biol. 106:2153 (1988).  
 SQ Sequence 15 AA;

Query Match 65.7%; Score 23; DB 1; Length 15;  
 Best Local Similarity 66.7%; Pred. No. 43;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VTQDDL 6  
 : : |||  
 Db 10 ICQDDL 15

## RESULT 17

W53913  
 ID W53913 standard; Peptide; 8 AA.

DT 17-AUG-1998 (first entry)  
 DE Interleukin-1 receptor accessory molecule K320-K327.  
 DE Interleukin-1 receptor accessory molecule; IL-1R ACN; human;  
 KW signal transduction; agonist; antagonist; antibody; infection;  
 KW septic shock; inflammation; rheumatoid arthritis; therapy; epitope;  
 KW antigen.

OS Homo sapiens.  
 PN W09808969-A1.  
 PD 05-MAR-1998.  
 PF 26-AUG-1996; U13954.  
 PR 26-AUG-1996; WO-U13954.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PI Bednarik DP, Olsen HS, Rosen CA;  
 DR WPI; 98-230267/20.

PT Nucleic acid encoding interleukin-1 receptor accessory protein -  
 used for therapeutic modulation of IL-1 activity  
 PS Claim 17; Page 83; 95pp; English.  
 CC This peptide corresponds to amino acids 320-327 of novel human  
 CC interleukin-1 receptor accessory molecule (IL1-R ACN) (see W53897),  
 CC a new member of the immunoglobulin superfamily that forms a complex  
 CC with type 1 IL1-R. It comprises an epitope-bearing portion of  
 CC IL1-R ACN. 18 Antigenic peptides comprising epitope-bearing  
 CC portions of human IL1-R ACN are claimed (see W53898-915). These  
 CC can be used to generate soluble IL1-R ACN-specific antibodies,  
 CC and may be produced by chemical synthesis or by recombinant means  
 CC using nucleic acid molecules (see V23659) of the invention. The  
 CC antibodies are useful as immunoassay reagents for detecting  
 CC IL1-R ACN, for affinity purification of IL1-R ACN and for  
 CC identifying cells that express IL1-R ACN.  
 SQ Sequence 8 AA;

Query Match 62.9%; Score 22; DB 1; Length 8;  
 Best Local Similarity 57.1%; Pred. No. 1.5e+05;  
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VTQDDLQ 7  
 : : |||  
 Db 2 VTSEDLK 8

## RESULT 18

W35486

ID W35486 standard; peptide; 12 AA.  
 AC W35486;

DT 22-APR-1998 (first entry)  
 DE Proteoglycan-associated lipoprotein peptide 1.  
 DE T-cell stimulatory peptide; immunogen; non-dendritic; carrier; tumour;  
 KW scaffold; inhibition; metastasis; wound healing; solid phase.  
 OS Actinobacillus pleuropneumoniae.  
 PN W09738011-A1.  
 PD 16-OCT-1997.  
 PF 03-APR-1997; D00146.  
 PR 03-APR-1996; DK-000398.  
 PA (PEPR-) PEPRESEARCH AS.  
 PI Heegaard PMH, Jakobsen PH;  
 DR WPI; 97-512645/47.  
 PT Non-dendritic peptide carrier linked to a solid phase - useful as a  
 PT diagnostic agent and as a scaffold for production of chemical  
 PT derivatives

PS Example 5; Page 89; 262pp; English.

CC A non-dendritic peptide carrier (A) has been developed which is coupled  
 CC through a linker to a solid phase, forming a complex of (A)-solid phase.  
 CC Where (A) comprises 10-50 amino acids capable of forming a secondary  
 CC structure in a benign buffer after liberation from the solid phase, and  
 CC further the (A)-solid phase complex comprises an immunogenic substance  
 CC and/or an immune mediator coupled on (A). The present sequence  
 CC represents a peptide used in an example from the present invention. An  
 CC (A)-solid phase complex can be used as a scaffold for the production of  
 CC chemical derivatives, characterised by covalently attaching molecules at  
 CC attachment points. Alternatively (A) is used as a scaffold-peptide for  
 CC the incorporation into an immunostimulating complex (iscom) resulting an  
 CC (A)-iscom complex which is used for the chemical coupling of antigenic  
 CC substances in an aqueous solution by conjugation. (A) derivatised with  
 CC one or more peptides having fibronectin-, laminin- or vitronectin-like  
 CC binding activities can be used for the promotion of cell-attachment to  
 CC plastic surfaces, in particular to inhibit tumour growth and metastasis,  
 CC and for promotion of wound healing. Also a derivatised (A) can be used  
 CC for the selection of specifically-binding aptamers or as a diagnostic  
 CC agent. Such diagnostic-(A) molecules could be used to detect molecules  
 CC derived from or indicative of pregnancy or of a disease, such as an  
 CC infectious, autoimmune or cancerous disease.  
 SQ Sequence 12 AA;

Query Match 62.9%; Score 22; DB 1; Length 12;  
 Best Local Similarity 57.1%; Pred. No. 54;  
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VTQDDLQ 7  
 : : |||  
 Db 2 MTAEDLQ 8

## RESULT 19

W35498

ID W35498 standard; peptide; 13 AA.

AC W35498;  
 DT 22-APR-1998 (first entry)  
 DE Pal A peptide from W09738011.  
 KW T-cell stimulatory peptide; immunogen; non-dendritic; carrier; tumour;  
 KW scaffold; inhibition; metastasis; wound healing; solid phase.  
 OS Unidentified.  
 PN W09738011-A1.  
 PD 16-OCT-1997.  
 PF 03-APR-1997; D00146.  
 PR 03-APR-1996; DK-000398.  
 PA (PEPR-) PEPRESEARCH AS.  
 PI Heegaard PMH, Jakobsen PH;  
 DR WPI; 97-512645/47.  
 PT Non-dendritic peptide carrier linked to a solid phase - useful as a  
 PT diagnostic agent and as a scaffold for production of chemical  
 PT derivatives

PS Example 7; Page 99; 262pp; English.

CC A non-dendritic peptide carrier (A) has been developed which is coupled  
 CC through a linker to a solid phase, forming a complex of (A)-solid phase.  
 CC Where (A) comprises 10-50 amino acids capable of forming a secondary  
 CC structure in a benign buffer after liberation from the solid phase, and

CC further the (A)-solid phase complex comprises an immunogenic substance  
 CC and/or an immune mediator coupled on (A). The present sequence  
 CC represents a peptide used in an example from the present invention. An  
 CC (A)-solid phase complex can be used as a scaffold for the production of  
 CC chemical derivatives, characterised by covalently attaching molecules at  
 CC attachment points. Alternatively (A) is used as a scaffold-peptide for  
 CC the incorporation into an immunostimulating Complex (Iscom) resulting in  
 CC (A)-Iscom complex which is used for the chemical coupling of antigenic  
 CC substances in an aqueous solution by conjugation. (A) derivatised with  
 CC one or more peptides having fibronectin-, laminin- or vitronectin-like  
 CC binding activities can be used for the promotion of cell-attachment to  
 CC plastic surfaces, in particular to inhibit tumour growth and metastasis,  
 CC and for promotion of wound healing. Also a derivatised (A) can be used  
 CC for the selection of specifically-binding aptamers or as a diagnostic  
 CC agent. Such diagnostic-(A) molecules could be used to detect molecules  
 CC derived from or indicative of pregnancy or of a disease, such as an  
 CC infectious, autoimmune or cancerous disease.  
 SQ Sequence 13 AA;

Query Match 62.9%; Score 22; DB 1; Length 13;  
 Best Local Similarity 57.1%; Pred. No. 59;  
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VTQDQLQ 7  
 Db 3 MTAEQLQ 9  
 ||:||

RESULT 20

ID W12358 standard; protein; 14 AA.  
 AC W12358;  
 DT 13-NOV-1997 (first entry)  
 DE Human hsp60 peptide p39 (343-366).  
 KW Heat-shock protein; hsp; hsp60; insulin-dependent diabetes mellitus;  
 KW IDDM.  
 OS Homo sapiens.  
 PN W09701959-A1.  
 PD 23-JAN-1997.  
 PF 01-JUL-1996; U11375.  
 PR 30-JUN-1995; IL-114407.  
 PA (YEDA ) YEDA RES & DEV CO LTD.  
 PI Abulafia R, Bockova J, Cohen IR, Elias D;  
 DR WPI: 97-108693/10.  
 DT New peptides) derived from human heat-shock protein 60 - used for  
 PT early diagnosis, prevention and treatment of insulin-dependent  
 PT diabetes mellitus  
 PS Claim 1: Page 13; 49pp; English.  
 CC The peptides given in W12346 to W12358 are derived from human hsp60  
 CC (W12345) and are useful for early diagnosis of IDDM by detecting,  
 CC in the blood or urine, antibodies or T-cells immunologically  
 CC reactive with human hsp60 (presence of which indicates high  
 CC probability of diabetes or its subsequent development).  
 CC Other peptides (W12359 to W12361) were shown not to be as  
 CC effective.  
 SQ Sequence 14 AA;

Query Match 62.9%; Score 22; DB 1; Length 14;  
 Best Local Similarity 80.0%; Pred. No. 65;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VTQDD 5  
 Db 8 VTKDD 12  
 ||:||

RESULT 21

W33050  
 ID W33050 standard; peptide; 14 AA.  
 AC W33050;  
 DT 26-JAN-1998 (first entry)

DE Human heat shock protein 60 residues 343-366.  
 KW Treatment; T cell mediated; disease; condition; antigen; human;  
 KW inflammatory T cell; pathogenesis; heat shock protein 60; hsp60;  
 KW insulin dependent diabetes mellitus; IDDM.  
 OS Homo sapiens.  
 PN W09702016-A1.  
 PD 23-JAN-1997.  
 PF 02-JUL-1996; U11373.  
 PR 05-JUL-1995; IL-114458.  
 PA (YEDA ) YEDA RES & DEV CO LTD.  
 PI Cohen IR, Elias D, Shinitzky M;  
 DR WPI: 97-108732/10.  
 DT Prepn. for treatment of T cell mediated diseases such as diabetes or  
 PT multiple sclerosis - comprises antigen recognised by inflammatory T  
 PT cells, and a fat emulsion carrier comprising e.g. soybean oil, egg  
 PT phospholipid and glycerol  
 PS Disclosure; Page 6; 39pp; English.  
 CC A preparation for the treatment of T cell mediated diseases or  
 CC conditions, comprises a carrier, comprising 10-20% triglycerides  
 CC and 1.2-2.4% phospholipids of plant and/or animal origin,  
 CC 2.25-4.5% osmo-regulator, 0-0.05% antioxidant and sterile water  
 CC (to 100 ml), and an antigen recognised by inflammatory T cells  
 CC associated with the pathogenesis of the disease or condition. The  
 CC preparation can be used to treat insulin dependent diabetes  
 CC mellitus, when the antigen is a peptide derived from heat shock  
 CC protein 60 (e.g. the present peptide). The emulsions promote a THI  
 CC to TH2 cytokine shift.  
 SQ Sequence 14 AA;

Query Match 62.9%; Score 22; DB 1; Length 14;  
 Best Local Similarity 80.0%; Pred. No. 65;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VTQDD 5  
 Db 8 VTKDD 12  
 ||:||

RESULT 22

R29290  
 ID R29290 standard; peptide; 6 AA.  
 AC R29290;  
 DT 07-APR-1993 (first entry)  
 DE Nerve growth stimulating protein fragment.  
 KW Ependymin; neuroactive domain; treatment; Huntington's chorea;  
 KW Parkinson's disease; Alzheimer's disease.  
 OS Synthetic.  
 PN W09220362-A.  
 PD 26-NOV-1992.  
 PF 14-MAY-1991; U03346.  
 PR 14-MAY-1991; WO-U03346.  
 PA (SHAS/) SHASHOUA VE.  
 PI Shashoua VE.  
 DR WPI: 92-415465/50.  
 DT Protein fragment comprising neuro-active domain of ependymin -  
 PT enhances nerve connectivity and growth and is for treating  
 PT nervous system disorders e.g. Huntington's, Parkinson's and  
 PT Alzheimer's diseases  
 PS Claim 21: Page 53; 77pp; English.  
 CC The fragment is that of an active region of the ependymin neuroactive  
 CC domain (gamma chain amino acids 164-169) effective in stimulating nerve  
 CC growth and elongation. It is 85.7% homologous to epidermal growth  
 CC factor amino acids 169-175. It can be used to treat nerve injuries  
 CC and to correct genetic or systemic disorders, e.g. treatment of  
 CC Huntington's, Parkinson's or Alzheimer's diseases, or to pretreat  
 CC nerve tissue before transplantation. It can be administered in  
 CC sustained release form and may be coupled to a carrier which protects  
 CC it against decomposition in the stomach and blood stream after oral  
 CC admin. and carries it across the blood brain barrier, opt. with  
 CC subsequent release of the free fragment in the brain.  
 SQ Sequence 6 AA;

Query Match 60.0%; Score 21; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDLQ 7  
|:|:|  
Db 1 DDLQ 4

RESULT 23  
ID W05563 standard; peptide: 6 AA.  
AC W05563;  
DT 09-DEC-1996 (first entry)  
DE Ependymin peptide fragment #8.  
KW Ependymin; nerve growth factor; glycoprotein; extracellular fluid; brain; cerebrospinal fluid; therapy; stroke recovery; neurodegenerative disease; neuron transplantation; memory loss; brain-penetration.  
OS Synthetic.  
PN US5545719-A.  
PD 13-AUG-1996.  
PF 01-MAY-1990; 517159.  
PR 01-MAY-1990; US-517159.  
PR 14-MAY-1991; US-700653.  
PR 24-FEB-1994; US-201046.  
PA (NEUR-) NEUROMEDICA INC.  
PI Shashoua VE;  
DR WPI; 96-383719/38.  
PT New ependymin peptide fragments - useful for promoting nerve growth  
PS Claim 1; Column 23; 19pp; English.  
CC W0556-W05583 represent fragments of the nerve growth factor ependymin.  
CC Ependymin is a glycoprotein dimer. The protein is synthesised by  
CC specific cells which secrete and maintain a steady state concentration of  
CC the protein in the extracellular and cerebrospinal fluids of the brain.  
CC Ependymin is a nerve growth promoter, but it is not currently known how  
CC it functions. These sequences promote nerve growth, and may be used as  
CC therapy to enhance recovery after stroke, to counteract age-related  
CC memory loss, or to treat neurodegenerative diseases. These sequences can  
CC also be used for research purposes, such as in neuron transplantation  
CC studies. Fatty acid conjugates of these peptides (using 16-22C fatty  
CC acids) have an increased brain-penetration index, and may be used for the  
CC same purposes.  
SQ Sequence 6 AA;

Query Match 60.0%; Score 21; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDLQ 7  
|:|:|  
Db 1 DDLQ 4

RESULT 24  
W97963  
ID W97963 standard; Peptide: 9 AA.  
AC W97963;  
DT 21-JUN-1999 (first entry)  
DE Human synaptonemal complex protein 1 (SCP-1) HLA binding motif.  
KW SCP-1; synaptonemal complex protein 1; human; spermatocyte;  
KW meiosis; tumour; marker; breast cancer; ovary cancer; glioma;  
KW renal cell carcinoma; transformed cell; diagnosis; therapy;  
KW vaccine; antibody; HLA; major histocompatibility complex; MHC.  
OS Homo sapiens.  
PN W0904040-A1.  
PD 28-JAN-1999.  
PF 25-JUN-1998; U13209.  
PR 15-JUL-1997; US-892702.  
PA (LUDW-) LUDWIG INST CANCER RES.  
PI Pfreundschuh M, Sahin U, Tureci O;  
DR WPI; 99-132280/11.

Query Match 60.0%; Score 21; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDLQ 7  
|:|:|  
Db 1 DDLQ 4

RESULT 24  
W97963  
ID W97963 standard; Peptide: 9 AA.  
AC W97963;  
DT 21-JUN-1999 (first entry)  
DE Human synaptonemal complex protein 1 (SCP-1) HLA binding motif.  
KW SCP-1; synaptonemal complex protein 1; human; spermatocyte;  
KW meiosis; tumour; marker; breast cancer; ovary cancer; glioma;  
KW renal cell carcinoma; transformed cell; diagnosis; therapy;  
KW vaccine; antibody; HLA; major histocompatibility complex; MHC.  
OS Homo sapiens.  
PN W0904040-A1.  
PD 28-JAN-1999.  
PF 25-JUN-1998; U13209.  
PR 15-JUL-1997; US-892702.  
PA (LUDW-) LUDWIG INST CANCER RES.  
PI Pfreundschuh M, Sahin U, Tureci O;  
DR WPI; 99-132280/11.

Query Match 60.0%; Score 21; DB 1; Length 9;  
Best Local Similarity 50.0%; Pred. No. 1.5e+05;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 TQDDLQ 7  
|:|:|  
Db 1 TEDDFE 6

RESULT 25  
W97904  
ID W97904 standard; Peptide: 10 AA.  
AC W97904;  
DT 21-JUN-1999 (first entry)  
DE Human synaptonemal complex protein 1 (SCP-1) HLA binding motif.  
KW SCP-1; synaptonemal complex protein 1; human; spermatocyte;  
KW meiosis; tumour; marker; breast cancer; ovary cancer; glioma;  
KW renal cell carcinoma; transformed cell; diagnosis; therapy;  
KW vaccine; antibody; HLA; major histocompatibility complex; MHC.  
OS Homo sapiens.  
PN W0904040-A1.  
PD 28-JAN-1999.  
PF 25-JUN-1998; U13209.  
PR 15-JUL-1997; US-892702.  
PA (LUDW-) LUDWIG INST CANCER RES.  
PI Pfreundschuh M, Sahin U, Tureci O;  
DR WPI; 99-132280/11.

Query Match 60.0%; Score 21; DB 1; Length 10;  
Best Local Similarity 50.0%; Pred. No. 71;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 TQDDLQ 7  
|:|:|  
Db 2 TEDDFE 7

RESULT 26  
R25221  
ID R25221 standard; Protein: 11 AA.

PT Detecting transformed cells from expression of synaptonemal complex  
PT protein - for diagnosis, prevention and treatment of cancer  
PS Example 6; Page 12; 37pp; English.  
CC This peptide corresponds to amino acids 42-50 the previously  
CC known human synaptonemal complex protein 1 (SCP-1), a protein  
CC that is involved in meiosis and which is expressed in tumour cells,  
CC especially in renal cell carcinomas, gliomas and breast carcinomas,  
CC but not in healthy cells except for testis. The peptide is  
CC presumed to bind to MHC molecule B44. It is one of 83 peptides (see  
CC W97901-83) derived from SCP-1 and identified as HLA binding motifs.  
CC Complexes formed between a peptide and an HLA molecule should  
CC provoke a cytolytic T cell response. The invention provides  
CC immunotherapeutic approaches to conditions characterised by  
CC aberrant or abnormal levels of one or more SCP proteins.  
SQ Sequence 9 AA;

Query Match 60.0%; Score 21; DB 1; Length 10;  
Best Local Similarity 50.0%; Pred. No. 71;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 TQDDLQ 7  
|:|:|  
Db 2 TEDDFE 7

RESULT 26  
R25221  
ID R25221 standard; Protein: 11 AA.

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AC R25221;
DE 23-DEC-1992 (first entry)
DE Residues 150-160 of mature apoE.
KW Inhibit lymphocyte proliferation; ovarian androgen secretion;
KW ovaries; low density lipoprotein receptor; LDL; steroidogenesis;
KW hepatic LDL-binding; autoimmune diseases; arthritis;
KW polycystic ovaries; hypercholesterolaemia.
OS Synthetic.
PN W09210512-A.
PD 25-JUN-1992.
PF 10-DEC-1991; U09269.
PR 10-DEC-1990; US-625093.
PR 30-SEP-1991; US-769629.
PR 09-DEC-1991; US-805193.
PA (SCRI) SCRIPPS RES INST.
PI Curtiss LK, Dyer CA, Smith R;
DR WPI; 92-234586/28.
PT Immunosuppressive polypeptide analogues of apolipoprotein E - for
PT modulating lymphocyte proliferation and ovarian androgen
PT synthesis, e.g. for treating inflammation, polycystic ovaries,
PT hypercholesterolaemia, and in diagnosis
PS Example 1; Page 59; 11pp; English.
CC This sequence was synthesised together with R25220-6 and a
CC lymphocyte cell culture system to examine the ability of various
CC polypeptides and conjugates to mimic the ability of apoE to inhibit
CC lymphocyte differentiation as evidence by proliferation. It was
CC found that they had no effect on lymphocyte proliferation when
CC used in nonconjugated monomeric form. However, when these
CC peptides were used conjugated to bovine serum albumin (BSA)
CC lymphocyte proliferation was inhibited in an equivalent manner by
CC all peptides studied as evidenced by decreasing amounts of
CC thymide uptake with increasing dose of conjugate. See also R25211-26.
SQ Sequence 11 AA;

Query Match 60.0%; Score 21; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDLQ 7
DB 4 DDLQ 7

RESULT 27
R88681
ID R88681 standard; Peptide; 14 AA.
AC R88681;
DE 19-AUG-1996 (first entry)
DE Allergen Alt a 45 T-cell epitope 1.
KW Alt a 45; Alt a 12; allergen; epitope; immunoglobulin E; IgE;
KW detection; immunotolerance; anergy.
OS Alternaria alternata.
PN AT9402038-A.
PD 15-NOV-1995.
PF 02-NOV-1994; 002038.
PR 02-NOV-1994; AT-002038.
PA (BIOM-) BIOMAY PRODN & HANDELSGES MBH.
PI Achatz G, Breitenbach M, Ebner C, Kraft D, Lechenauer E;
PI Oberkofler H, Prillinger H, Simon B, Unger A;
DR WPI; 96-040555/05.
PT Recombinant DNA encoding allergens of Alternaria alternata - useful
PT in diagnosis and treatment of A. alternata allergies
PS Claim 1; Page 11; 21pp; German.
CC R88681-91 are T-cell epitopes derived from the Alt a 45 allergen protein
CC (R88672) isolated from Alternaria alternata. Peptide epitopes from Alt a
CC 45 and Alt a 12 (R88692) are useful as diagnostic reagents, e.g. for in
CC vitro detection of allergy caused by Alt a 45 and 12 (by reaction with
CC IgE in serum). They can also detect cellular reaction to the specified
CC allergens (from their stimulatory or inhibitory effect on this reaction).
CC The peptides can also be used therapeutically to induce immunotolerance
CC or anergy of T lymphocytes.
SQ Sequence 14 AA;

Query Match 60.0%; Score 21; DB 1; Length 14;
Best Local Similarity 60.0%; Pred. No. 1e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 TQDDL 6
DB 3 TEDDM 7

RESULT 29
W81217
ID W81217 standard; peptide; 6 AA.
AC W81217;
DE 30-APR-1999 (first entry)
DE Human iNOS peptide fragment PS-5246.
KW Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;
KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;
KW myocardial infarction; tissue rejection; transplantation; psoriasis;
KW autoimmune disease; multiple sclerosis.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Modified_site 6 /note= "Asp residue amidated"
FT W09845710-Al.
PN 15-OCT-1998.
PF 11-APR-1997; U06500.
PR 07-APR-1997; US-667777.

Query Match 60.0%; Score 21; DB 1; Length 14;
Best Local Similarity 57.1%; Pred. No. 1e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VTQDDLQ 7
DB 4 VTKDTLE 10

RESULT 28
W30922
ID W30922 standard; peptide; 14 AA.
AC W30922;
DE 08-JAN-1998 (first entry)
DE Birch pollen allergen B cell epitope.
DE Cofactor-independent phosphoglycerate mutase; PGM-i; E.C. 5.4.21;
KW Birch; pollen; allergy; plant allergen; panallergen; B cell;
KW T cell; epitope; immunotherapy; detection; diagnosis;
KW hay fever; conserved.
OS Betula verrucosa.
PN W09705258-A2.
PD 13-FEB-1997.
PF 02-AUG-1996; AT0141.
PR 02-AUG-1995; AT-001320.
PA (BIOM-) BIOMAY PRODN & HANDELS GMBH.
PI Breitenbach M, Ebner C, Engel E, Ferreira F, Jilek A;
PI Kraft D, Richter K, Rheinberger H;
DR WPI; 97-145695/13.
PT New recombinant DNA encoding plant phosphoglycerate mutase or its
PT antigenic epitope(s) - useful for diagnosis or treatment of
PT allergies to pollen and plant-derived foods
PS Disclosure; Fig 3; 16pp; German.
CC W30920-W30935 are B cell epitopes of a birch pollen co-factor-independent
CC phosphoglycerate mutase (PGM-i) allergen. PGM-i is a highly conserved
CC plant allergen (panallergen) which can cause cross-reactivity in
CC patients allergic to pollen and plant-derived foods. PGM-i and it's B
CC cell and T cell epitopes can be used for the in vitro detection of
CC allergy against PGM-i, by measuring serum IgE or a cellular reaction.
CC They can also be used in immunotherapy and will not cause an autoimmune
CC response because PGM-i is significantly different from the human
CC enzyme, which is co-factor dependent.
SQ Sequence 14 AA;

```

QY 1 VTQD 4  
Db 3 VTQD 6

Search completed: June 30, 2000, 14:52:32  
Job time: 5999 sec

PA (WEBB/) WEBBER R.  
PI Webber R;  
DR WPI: 98-594495/50.  
PT Detection of human inducible nitric oxide synthase - using an  
PT immunoassay in which a sample is contacted with a specific binding  
PT entity reactive with human iNOS or mimics.  
PS Example 4; Page 34; 93pp; English.  
CC This invention describes an immunoassay method where a sample with a  
CC specific binding entity (e.g. a monoclonal antibody) reactive to human  
CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used  
CC to detect the presence of human iNOS protein in the sample. The method  
CC can be used for the detection and quantitation of human iNOS in cells and  
CC tissues for various pathological conditions such as sepsis, septic  
CC shock, myocardial infarction, rejection of tissue in organs following  
CC transplantation, monitoring "flare ups" in certain autoimmune diseases  
CC such as lupus, psoriasis, and multiple sclerosis. This sequence  
CC represents a peptide from human iNOS which is used in the method of the  
CC invention.  
SQ Sequence 6 AA;

Query Match 57.1%; Score 20; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VTQD 4  
Db 3 VTQD 6

RESULT 30  
W81230  
ID W81230 standard; peptide; 6 AA.  
AC W81230;  
DT 30-APR-1999 (first entry)  
DE Human iNOS peptide fragment PS-5268.  
KW Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;  
KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;  
KW myocardial infarction; tissue rejection; transplantation; psoriasis;  
KW autoimmune disease; multiple sclerosis.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT Modified\_site 6 /note- "Asp residue amidated"  
PN WC9845710-A1.  
PD 15-OCT-1998.  
PF 11-APR-1997; U06500.  
PR 07-APR-1997; US-667777.  
PA (WEBB/) WEBBER R.  
PI Webber R;  
DR WPI: 98-594495/50.  
PT Detection of human inducible nitric oxide synthase - using an  
PT immunoassay in which a sample is contacted with a specific binding  
PT entity reactive with human iNOS or mimics.  
PS Example 4; Page 36; 93pp; English.  
CC This invention describes an immunoassay method where a sample with a  
CC specific binding entity (e.g. a monoclonal antibody) reactive to human  
CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used  
CC to detect the presence of human iNOS protein in the sample. The method  
CC can be used for the detection and quantitation of human iNOS in cells and  
CC tissues for various pathological conditions such as sepsis, septic  
CC shock, myocardial infarction, rejection of tissue in organs following  
CC transplantation, monitoring "flare ups" in certain autoimmune diseases  
CC such as lupus, psoriasis, and multiple sclerosis. This sequence  
CC represents a peptide from human iNOS which is used in the method of the  
CC invention.  
SQ Sequence 6 AA;

Query Match 57.1%; Score 20; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: June 30, 2000, 13:27:55 ; Search time 50.08 Seconds

(without alignments)

8.195 Million cell updates/sec

Title: US-08-833-506C-89

Perfect score: 35

Sequence: 1 VTQDDLQ 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 168808 seqs, 58629743 residues

Total number of hits satisfying chosen parameters: 2577

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Listing first 100 summaries

Database : PIR\_63:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	60.0	7	2	S68004
2	57.1	12	2	13	I39390
3	20	57.1	15	2	E56819
4	20	57.1	15	2	A53594
5	19	54.3	11	2	S42449
6	18	51.4	12	2	B58503
7	18	51.4	14	2	A61002
8	17	48.6	13	2	A23694
9	17	48.6	13	2	A57789
10	17	48.6	15	2	PS0218
11	17	48.6	15	2	B48047
12	16	45.7	8	2	I40697
13	16	45.7	4	3	PC4131
14	16	45.7	11	2	PH0904
15	16	45.7	12	2	S53681
16	16	45.7	12	2	S39762
17	16	45.7	13	2	S41209
18	16	45.7	13	2	PS0443
19	16	45.7	14	2	S29789
20	16	45.7	15	2	PA0110
21	16	45.7	15	2	B32800
22	16	45.7	15	2	C32521
23	16	45.7	15	2	B26501
24	15	42.9	9	2	PW0002
25	15	42.9	10	2	SL3224
26	15	42.9	13	2	S15755
27	15	42.9	14	2	A41589
28	15	42.9	14	2	I49514
29	15	42.9	15	2	I58116
30	15	42.9	15	2	PH1310
					huclin, 75K chain
					acetylcholine rece
					PS I complex subun
					calnexin - mouse (
					anti protein - pha
					outer membrane por
					photosystem II oxy
					myosin heavy chain
					galbladder stone
					24K protein 4413 -
					phospholipase C-be
					biotin A - Citroba
					hypothetical 8 pro
					T-cell receptor be
					Yolk glycoprotein
					cytochrome P450 ut
					F420-non-reducing-
					potassium channel
					hypothetical prote
					translation elonga
					hypothetical prote
					hexokinase (EC 2.7
					lipoprotein lipase
					chlorophyll a/b-bi
					virG protein - Agr
					actin 7 - soybean
					25K elastin-bindin
					B144 protein A - m
					Dpil6 - human
					Ig heavy chain DJ

30K protein - bovi  
Ig heavy chain V r  
neuropeptide TE-6  
opacity protein P.  
calsequestrin, fas  
trypsin (EC 3.4.21  
unidentified 4.5/4  
neurotoxin-associa  
type II site-speci  
31K protein 3208 -  
variant surface gl  
multicatalytic end  
heat-shock protein  
beta-glucosidase (   
T cell receptor al  
glycoprotein compo  
tubulin beta-3 cha  
alpha-globulin - r  
GTP-binding protei  
fibrinopeptide A -  
insulin-like growt  
Ig H chain V-D-J r  
T-cell receptor de  
bone acidic glycop  
light-harvesting p  
T-cell receptor be  
T-cell receptor be  
T-cell receptor be  
T-cell receptor be  
fibroblast growth  
T-cell receptor be  
calliFMRamide 9 -  
ornithine decarbox  
H-hyosporin - Ja  
T-cell receptor be  
lignin peroxidase  
lignin peroxidase  
Ig kappa chain V-I  
Ig kappa chain V-I  
ribosomal protein  
chlorophyll a/b-bi  
Ig H chain V-D-J r  
T-cell receptor be  
integration host f  
ennatiin synthetas  
fumarate hydratase  
protein QF200051 -  
serine proteinase  
agrin - electric r  
glycoprotein - log  
T cell receptor V -  
collagen type I -  
Tcr delta chain V -  
epidermal growth f  
T-cell receptor be  
hypothetical 6 pro  
cerbellar degener  
formylglycinamide  
T-cell receptor be  
tocopherol-binding  
ferridoxin a2 - Ja  
calliFMRamide 2 -  
calliFMRamide 3 -  
late G1-69 protein  
leucosulfakinin-II

ALIGNMENTS

```

RESULT 1
S68004
C:Title: 75K chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C:Accession: S68004
R:Edgar, P.F.
FEBS Lett. 375, 159-161, 1995
A:Title: Hucolin, a new corticosteroid-binding protein from human plasma with structural
A:Reference number: S68004; MUID:56087107
A:Accession: S68004
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <EDG>

Query Match 50.0%; Score 21; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDLQ 7
Db 4 DDLQ 7

RESULT 2
I39390
C:Title: acetylcholine receptor (alternative exon 5b) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 30-May-1997
C:Accession: I39390
R:Mihovilovic, M.; Mai, Y.; Herbstreith, M.; Rubboli, F.; Tarroni, P.; Clementi, F.; Ros
Biochem. Biophys. Res. Commun. 197, 137-144, 1993
A:Title: Splicing of an anti-sense Alu sequence generates a coding sequence variant for
A:Reference number: I39390; MUID:94071933
A:Accession: I39390
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-12 <RES>
A:Cross-references: GB:L18973; NID:g441143; PID:g441144
C:Keywords: alternative splicing; neurotransmitter receptor

Query Match 57.1%; Score 20; DB 2; Length 12;
Best Local Similarity 57.1%; Pred. No. 2e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VTQDDLQ 7
Db 6 VTQGVQ 12

RESULT 3
PS I complex subunit 8 - cucumber (fragment)
C:Species: Cucumis sativus (cucumber)
C:Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 05-Jan-1996
C:Accession: E56819
R:Iwasaki, Y.; Ishikawa, H.; Hibino, T.; Takabe, T.
Biochim. Biophys. Acta 1059, 141-148, 1991
A:Title: Characterization of genes that encode subunits of cucumber PS I complex by N-te
A:Reference number: A56819; MUID:91355209
A:Accession: E56819
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <IWA>
A>Note: sequence extracted from NCBI backbone (NCBI:P:58606)

Query Match 57.1%; Score 20; DB 2; Length 15;
Best Local Similarity 80.0%; Pred. No. 2.5e+02;


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Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VTQDD 5
Db 10 VIQDD 14

RESULT 4
A53594
C:Title: calnexin - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 01-Dec-1995 #sequence_revision 01-Dec-1995 #text_change 17-Mar-1999
C:Accession: A53594
R:Lenter, M.; Vestweber, D.
J. Biol. Chem. 269, 12263-12268, 1994
A:Title: The integrin chains beta-1 and alpha-6 associate with the chaperone calnexin
A:Reference number: A53594; MUID:94216347
A:Accession: A53594
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <LEN>
C:Keywords: endoplasmic reticulum; molecular chaperone

Query Match 57.1%; Score 20; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 2.5e+02;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VTQDDL 6
Db 10 IIEDDL 15

RESULT 5
S42449
C:Title: anti protein - phage P7
C:Species: phage P7
C:Date: 07-Sep-1994 #sequence_revision 26-May-1995 #text_change 08-Oct-1999
C:Accession: S42449
R:Citron, M.; Schuster, H.
Cell 62, 591-598, 1990
A:Title: The c4 repressors of bacteriophages P1 and P7 are antisense RNAs.
A:Reference number: S42448; MUID:90335968
A:Accession: S42449
A>Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-11 <CT>
A:Cross-references: EMBL:M35139; NID:g215705; PIDN:AAA32437.1; PID:g215707

Query Match 54.3%; Score 19; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 2.9e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VTQDDL 6
Db 6 VTRNDI 11

RESULT 6
B58503
C:Title: outer membrane porin protein OprD homolog - unidentified bacterium (fragment)
N:Alternate names: 43K bile stone protein
C:Species: unidentified bacterium
C:Date: 07-Feb-1997 #sequence_revision 07-Feb-1997 #text_change 10-Jul-1998
C:Accession: B58503
R:Binette, J.P.; Binette, M.B.
submitted to the Protein Sequence Database, October 1996
A:Description: The proteins of kidney and gallbladder stones.
A:Reference number: A58501
A:Accession: B58503
A>Status: preliminary
A:Molecule type: protein

```



A:Residues: 1-12 <BIN>  
A:Experimental source: human bile with stones  
A:Note: sequenced along with secondary sequence MXIGVNEXL

Query Match 51.4%; Score 18; DB 2; Length 12;  
Best Local Similarity 75.0%; Pred. No. 5.2e+02;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 TQDD 5  
: : : :  
Db 2 SQDD 5

RESULT 7  
A61002  
Photosystem II oxygen-evolving complex protein 1 - common tobacco (fragment)  
N:Alternate names: thylakoid membrane protein  
C:Species: Nicotiana tabacum (common tobacco)  
C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 17-Mar-1999  
A:Accession: A61002  
R:Baum, G.; Rasmussen, H.H.; Van Den Bulcke, M.; Van Damme, J.; Puype, M.; Gesser, B.; C  
Electrophoresis 11, 528-536, 1990  
A:Title: Two-dimensional gel electrophoresis, protein electroblotting and microsequencing  
A:Reference number: A61002; MUID:91031404  
A:Accession: A61002  
A:Molecule type: protein  
A:Residues: 1-14 <BAU>  
C:Keywords: chloroplast; membrane protein; photosynthesis; photosystem II; thylakoid

Query Match 51.4%; Score 18; DB 2; Length 14;  
Best Local Similarity 42.9%; Pred. No. 6.2e+02;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 VTQDDIQ 7  
: : : :  
Db 7 LTFDEIQ 13

RESULT 8  
A23694  
Myosin heavy chain, smooth muscle - chicken (fragment)  
C:Species: Gallus gallus (chicken)  
C:Date: 04-Oct-1991 #sequence\_revision 04-Oct-1991 #text\_change 07-Feb-1997  
C:Accession: A23694  
R:Cole, D.G.; Yount, R.G.  
J. Biol. Chem. 265, 22537-22546, 1990  
A:Title: Photolabeling of the 6 and 10 S conformations of gizzard myosin with 3'-(2')-O-(  
A:Reference number: A23694; MUID:91093105  
A:Accession: A23694  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-13 <COL>  
C:Keywords: smooth muscle

Query Match 48.6%; Score 17; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 9.3e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QDD 5  
: : : :  
Db 11 QDD 13

RESULT 9  
A57789  
gallbladder stone matrix protein 1, 41K - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 23-Feb-1996 #sequence\_revision 23-Feb-1996 #text\_change 03-May-1996  
A:Accession: A57789  
R:Binette, J.P.; Binette, M.B.

submitted to the Protein Sequence Database, February 1996  
A:Description: The proteins of gallbladder stones.  
A:Reference number: A57789  
A:Accession: A57789  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-13 <BIN>  
A:Experimental source: two gallbladder, one bladder, one kidney stone of different pa  
A:Note: 9-Leu and 12-Lys were also found

Query Match 48.6%; Score 17; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 9.3e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QDD 5  
: : : :  
Db 3 QDD 5

RESULT 10  
PS0218  
24K protein 4413 - rice (strain Nihonbare) (fragment)  
N:Alternate names: unidentified protein QR310029  
C:Species: Oryza sativa (rice)  
C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 23-Aug-1997  
A:Accession: PS0218; PC4270  
R:Tsugita, A.  
submitted to JIPID, April 1993  
A:Reference number: PS0206  
A:Accession: PS0218  
A:Molecule type: protein  
A:Residues: 1-15 <TSU>  
A:Experimental source: strain Nihonbare  
R:Kawakami, T.; Kamo, M.; Chen, M.C.; Tsugita, A.  
submitted to JIPID, April 1997  
A:Reference number: PC4267  
A:Accession: PC4270  
A:Molecule type: protein  
A:Residues: 1-15 <RAW>

Query Match 48.6%; Score 17; DB 2; Length 15;  
Best Local Similarity 75.0%; Pred. No. 1.1e+03;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VTQD 4  
: : : :  
Db 1 LTQD 4

RESULT 11  
B48047  
phospholipase C-beta 4, PLC-beta - bovine (fragment)  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 07-Apr-1994 #sequence\_revision 18-Nov-1994 #text\_change 23-Mar-1995  
C:Accession: B48047  
R:Lee, C.W.; Park, D.J.; Lee, K.H.; Kim, C.G.; Rhee, S.G.  
J. Biol. Chem. 268, 21318-21327, 1993  
A:Title: Purification, molecular cloning, and sequencing of phospholipase C-beta 4.  
A:Reference number: A48047; MUID:94012887  
A:Accession: B48047  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-15 <LEE>  
A:Experimental source: retina  
A:Note: sequence extracted from NCBI backbone (NCBIP:138522)

Query Match 48.6%; Score 17; DB 2; Length 15;  
Best Local Similarity 57.1%; Pred. No. 1.1e+03;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 VTQDDLQ 7  
| | : | |  
Db 3 VTVEDEQ 9

RESULT 12  
I40697  
biotin A - Citrobacter freundii (fragment)  
C:Species: Citrobacter freundii  
C:Date: 12-Aug-1996 #sequence\_revision 12-Aug-1996 #text\_change 12-Aug-1996  
C:Accession: I40697  
R:Shiuan, D.; Campbell, A.  
Gene 67, 203-211, 1988  
A:Title: Transcriptional regulation and gene arrangement of Escherichia coli, Citrobacter  
A:Reference number: I40697; MUID:89006280  
A:Accession: I40697  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-4 <RES>  
A:Cross-references: GB:M21922; NID:g144434

Query Match 45.7%; Score 16; DB 2; Length 4;  
Best Local Similarity 75.0%; Pred. No. 1.7e+05;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TODD 5  
| | |  
Db 1 TTDD 4

RESULT 13  
PC4131  
hypothetical 8 protein - Pseudomonas aeruginosa (fragment)  
C:Species: Pseudomonas aeruginosa  
C:Date: 03-Sep-1998 #sequence\_revision 03-Sep-1998 #text\_change 03-Sep-1998  
C:Accession: PC4131  
R:Kawasaki, S.; Arai, H.; Igarashi, Y.; Kodama, T.  
Gene 167, 87-91, 1995  
A:Title: Sequencing and characterization of the downstream region of the genes encoding  
Y for biosynthesis of heme d1  
A:Reference number: JC4552; MUID:96144254  
A:Accession: PC4131  
A:Status: preliminary  
A:Residues: 1-8 <KAW>  
A:Cross-references: DBJ:D50473

Query Match 45.7%; Score 16; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDL 6  
| | |  
Db 2 DDL 4

RESULT 14  
PH0904  
T-cell receptor beta chain V-D-J region (hybridoma S22C2) - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 30-May-1997  
C:Accession: PH0904  
R:Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.  
J. Exp. Med. 174, 1467-1476, 1991  
A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic  
A:Reference number: PH0891; MUID:92078857  
A:Accession: PH0904  
A:Molecule type: mRNA  
A:Residues: 1-11 <GOL>  
A:Experimental source: myelin basic protein-immunized T-cell  
C:Keywords: T-cell receptor

Query Match 45.7%; Score 16; DB 2; Length 11;  
Best Local Similarity 50.0%; Pred. No. 1.3e+03;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 TQDDLQ 7  
: | | |  
Db 3 SPSDSLQ 8

RESULT 15  
S55681  
yolk glycoprotein 42k - chicken  
C:Species: Gallus gallus (chicken)  
C:Date: 28-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 07-May-1999  
C:Accession: S55681  
R:Yamamura, J.; Adachi, T.; Aoki, N.; Nakajima, H.; Nakamura, R.; Matsuda, T.  
Biochim. Biophys. Acta 1244, 384-394, 1995  
A:Title: Precursor-product relationship between chicken vitellogenin and the yolk pro  
A:Reference number: S55680; MUID:95322425  
A:Accession: S55681  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-12 <YAM>  
C:Keywords: glycoprotein

Query Match 45.7%; Score 16; DB 2; Length 12;  
Best Local Similarity 40.0%; Pred. No. 1.4e+03;  
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VTQDD 5  
: | |  
Db 7 IQAED 11

RESULT 16  
S39762  
cytochrome P450 UT-7b - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 19-May-1994 #sequence\_revision 10-Nov-1995 #text\_change 10-Nov-1995  
C:Accession: S39762  
R:Ohishi, N.; Imaoka, S.; Suzuki, T.; Funae, Y.  
Biochim. Biophys. Acta 1158, 227-236, 1993  
A:Title: Characterization of two P-450 isozymes placed in the rat CYP2D subfamily.  
A:Reference number: S39761; MUID:94072607  
A:Accession: S39762  
A:Molecule type: protein  
A:Residues: 1-12 <OHI>

Query Match 45.7%; Score 16; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDL 6  
| | |  
Db 6 DDL 8

RESULT 17  
S41209  
F420-non-reducing-hydrogenase (EC 1.12.99.-) 17K chain - Methanobacterium thermoautot  
C:Species: Methanobacterium thermoautotrophicum  
A:Variety: Strain Marburg  
C:Date: 06-Feb-1995 #sequence\_revision 17-Jul-1998 #text\_change 07-May-1999  
C:Accession: S41209  
R:Setzke, E.; Hedderich, R.; Heiden, S.; Thauer, R.K.  
Eur. J. Biochem. 220, 139-148, 1994  
A:Title: H(2): heterodisulfide oxidoreductase complex from Methanobacterium thermoaut  
A:Reference number: S41204; MUID:94164153

A:Accession: S41209  
A:Molecule type: protein  
A:Residues: 1-13 <SET>  
A:Experimental source: strain Marburg  
C:Complex: membrane-associated complex; holoenzyme is the hydrogen:heterodisulfide oxidoreductase (EC 1.12.99.2) and a F420-non-reducing-hydrogenase (EC 1.12.99.-) subcomplex; each of the subcomplexes (EC 1.12.99.2)  
C:Function:  
A:Description: reduction of coenzyme M-N-7-mercaptoheptanoylthreonine phosphate heterodisulfide (EC 1.12.99.2)  
C:Keywords: membrane-associated complex; oxidoreductase

Query Match 45.7%; Score 16; DB 2; Length 13;  
Best Local Similarity 50.0%; Pred. No. 1.5e+03;  
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 QDDL 6  
DB 2 EDDI 5

RESULT 18  
PS0443  
potassium channel protein Slo G3 - fruit fly (Drosophila melanogaster) (fragment)  
C:Species: Drosophila melanogaster  
C:Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 16-Feb-1997  
C:Accession: PS0443  
R:Adelman, J.P.; Shen, K.Z.; Kavanaugh, M.P.; Warren, R.A.; Wu, Y.N.; Lagrutta, A.; Bond  
Neuron 9, 209-216, 1992  
A:Title: Calcium-activated potassium channels expressed from cloned complementary DNAs.  
A:Reference number: JH0697; MUID:92360298  
A:Accession: PS0443  
A>Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-13 <ADE>  
C:Comment: This potassium channel is activated by calcium.  
C:Genetics:  
A:Gene: FlyBase:slo  
A:Cross-references: FlyBase:FBgn0003429  
C:Keywords: alternative splicing; ion channel; potassium channel; transmembrane protein

Query Match 45.7%; Score 16; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDL 6  
DB 10 DDL 12

RESULT 19  
S29789  
hypothetical protein - Thermoplasma acidophilum (fragment)  
C:Species: Thermoplasma acidophilum  
C:Date: 25-Feb-1994 #sequence\_revision 26-May-1995 #text\_change 26-May-1995  
C:Accession: S29789  
R:Bright, J.R.; Byrom, D.; Danson, M.J.; Hough, D.W.; Towner, P.  
Eur. J. Biochem. 211, 549-554, 1993  
A:Title: Cloning, sequencing and expression of the gene encoding glucose dehydrogenase from Thermoplasma acidophilum  
A:Reference number: S29788; MUID:93170285  
A:Accession: S29789  
A>Status: Preliminary  
A:Molecule type: DNA  
A:Residues: 1-14 <BRI>  
A:Cross-references: EMBL:X59788

Query Match 45.7%; Score 16; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDL 6

DB 9 DDL 11

RESULT 20

PA0110  
translation elongation factor eEF-1 beta' chain - Arabidopsis thaliana (fragment)  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 07-Apr-1995 #sequence\_revision 26-May-1995 #text\_change 26-Apr-1996  
C:Accession: PA0110  
R:Kamo, M.; Kawakami, T.; Tsugita, A.  
submitted to JIPID, March 1995  
A:Reference number: PA0109  
A:Accession: PA0110  
A:Molecule type: protein  
A:Residues: 1-15 <RAM>

Query Match 45.7%; Score 16; DB 2; Length 15;  
Best Local Similarity 66.7%; Pred. No. 1.8e+03;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 VTODDL 6  
DB 2 VTFSDL 7

RESULT 21  
B32800  
hypothetical protein (p1 5' region) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 22-Nov-1989 #sequence\_revision 22-Nov-1989 #text\_change 30-Sep-1993  
C:Accession: B32800  
R:Jindal, S.; Dudani, A.K.; Singh, B.; Harley, C.B.; Gupta, R.S.  
Mol. Cell. Biol. 9, 2279-2283, 1989  
A:Title: Primary structure of a human mitochondrial protein homologous to the bacteriophage T4 gp105  
A:Reference number: A32800; MUID:89313783  
A:Accession: B32800  
A>Status: Preliminary  
A:Molecule type: mRNA  
A:Residues: 1-15 <JIN>  
A:Cross-references: GB:M22382

Query Match 45.7%; Score 16; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDL 6  
DB 1 DDL 3

RESULT 22  
C32521  
hexokinase (EC 2.7.1.1) I peptide II - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 28-Apr-1993  
C:Accession: C32521  
R:Schirch, D.M.; Willson, J.E.  
Arch. Biochem. Biophys. 257, 1-12, 1987  
A:Title: Rat brain hexokinase: amino acid sequence at the substrate hexose binding site  
A:Reference number: A90080; MUID:87324917  
A:Accession: C32521  
A:Molecule type: protein  
A:Residues: 1-15 <SCH>  
C:Keywords: glycolysis; phosphotransferase

Query Match 45.7%; Score 16; DB 2; Length 15;  
Best Local Similarity 75.0%; Pred. No. 1.8e+03;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TODD 5  
| | |  
Db 11 TXDD 14

RESULT 23  
B26501  
lipoprotein lipase (EC 3.1.1.34) - guinea pig (fragment)  
C:Species: Cavia porcellus (guinea pig)  
C:Date: 21-May-1988 #sequence\_revision 21-May-1988 #text\_change 28-Apr-1993  
C:Accession: B26501  
R:Bengtsson-Oliverona, G.; Oliverona, T.; Jorvall, H.  
Eur. J. Biochem. 161, 281-288, 1986  
A:Title: Lipoprotein lipases from cow, guinea-pig and man. Structural characterization of  
A:Reference number: A91178; MUID:87054027  
A:Accession: B26501  
A:Molecule type: protein  
A:Residues: 1-15 <BEN>  
C:Keywords: carboxylic ester hydrolase

Query Match 45.7%; Score 16; DB 2; Length 15;  
Best Local Similarity 50.0%; Pred. No. 1.8e+03;  
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDLQ 7  
| | |  
Db 8 DDIE 11

RESULT 24  
PW0002  
chlorophyll a/b-binding protein 31K - green alga (Dunaliella tertiolecta) (fragment)  
N:Alternate names: photosystem II light-harvesting chlorophyll 31K protein  
C:Species: Dunaliella tertiolecta  
C:Date: 24-Nov-1999 #sequence\_revision 24-Nov-1999 #text\_change 24-Nov-1999  
C:Accession: PW0002  
R:LaRoche, J.; Bennett, J.; Falkowski, P.G.  
Gene 95, 165-171, 1990  
A:Title: Characterization of a cDNA encoding for the 28.5-kDa LHClI apoprotein from the  
A:Reference number: JW0040; MUID:91065528  
A:Accession: PW0002  
A:Molecule type: protein  
A:Residues: 1-9 <LAK>  
C:Superfamily: chlorophyll a/b-binding protein  
C:Keywords: chloroplast; grana; light-harvesting complex; membrane adhesion; membrane pr

Query Match 42.9%; Score 15; DB 2; Length 9;  
Best Local Similarity 50.0%; Pred. No. 1.7e+05;  
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDLQ 7  
| | |  
Db 4 DEMQ 7

RESULT 25  
S13224  
virG protein - Agrobacterium sp. (fragment)  
C:Species: Agrobacterium sp.  
C:Date: 19-Mar-1997 #sequence\_revision 01-Aug-1997 #text\_change 01-Aug-1997  
C:Accession: S13224  
R:Tamamoto, S.; Aoyama, T.; Takanami, M.; Oka, A.  
J. Mol. Biol. 215, 537-547, 1990  
A:Title: Binding of the regulatory protein VirG to the phased signal sequences upstream  
A:Reference number: S13224; MUID:91039316  
A:Accession: S13224  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-10 <TAM>

Query Match 42.9%; Score 15; DB 2; Length 10;  
Best Local Similarity 60.0%; Pred. No. 1.8e+03;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 VTODD 5  
| | |  
Db 6 VIDDD 10

RESULT 26  
S15755  
actin 7 - soybean (fragment)  
C:Species: Glycine max (soybean)  
C:Date: 20-Feb-1995 #sequence\_revision 29-May-1998 #text\_change 13-Aug-1999  
C:Accession: S15755  
R:Pearson, L.; Meagher, R.B.  
Plant Mol. Biol. 14, 513-526, 1990  
A:Title: Diverse soybean actin transcripts contain a large intron in the 5' untransla  
A:Reference number: S15754; MUID:91346640  
A:Accession: S15755  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-13 <PEA>  
A:Cross-references: EMBL:X17120; NID:g18527; PIDN:CAA34980.1; PID:g18528  
C:Superfamily: actin  
C:Keywords: cytoskeleton; structural protein

Query Match 42.9%; Score 15; DB 2; Length 13;  
Best Local Similarity 50.0%; Pred. No. 2.5e+03;  
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDLQ 7  
| | |  
Db 5 EDIQ 8

RESULT 27  
A41589  
25K elastin-binding protein - Staphylococcus aureus (fragment)  
C:Species: Staphylococcus aureus  
C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 23-Mar-1993  
C:Accession: A41589  
R:Park, P.W.; Roberts, D.D.; Grosso, L.E.; Parks, W.C.; Rosenbloom, J.; Abrams, W.R.;  
J. Biol. Chem. 266, 23399-23406, 1991  
A:Title: Binding of elastin to Staphylococcus aureus.  
A:Reference number: A41589; MUID:92078218  
A:Accession: A41589  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-14 <PAR>

Query Match 42.9%; Score 15; DB 2; Length 14;  
Best Local Similarity 40.0%; Pred. No. 2.7e+03;  
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 QDDLQ 7  
| | |  
Db 5 KDDFE 9

RESULT 28  
I49514  
B144 protein A - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 05-Nov-1999  
C:Accession: I49514  
R:Tsuze, I.; Shen, F.  
Immunogenetics 26, 378-380, 1987  
A:Title: A gene in the H-2S: H-2D interval of the major histocompatibility complex wh  
A:Reference number: I49514; MUID:88031493  
A:Accession: I49514

A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-14 <RES>  
A:Cross-references: GB:M18187; NID:g192097; PIDN:AAA37272.1; PID:g192098

Query Match 42.9%; Score 15; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 DLQ 7  
| | |  
Db 3 DLQ 5

RESULT 29  
I58116  
Dp116 - human  
C:Species: Homo sapiens (man)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 13-Aug-1999  
C:Accession: I58116  
R:Byers, T.J.; Lidov, H.G.; Kunkel, L.M.  
Nature Genet. 4, 77-81, 1993  
A:Title: An alternative dystrophin transcript specific to peripheral nerve.  
A:Reference number: I58116; MUID:93291881  
A:Accession: I58116  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-15 <RES>  
A:Cross-references: GB:S62617; NID:g386224; PIDN:AAB27159.1; PID:g386225  
C:Superfamily: dystrophin; alpha-actinin actin-binding domain homology; spectrin/dystroph

Query Match 42.9%; Score 15; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 DLQ 7  
| | |  
Db 11 DLQ 13

RESULT 30  
PH1310  
Ig heavy chain DJ region (clone C770-107) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
C:Accession: PH1310  
R:Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.  
J. Exp. Med. 176, 1577-1581, 1992  
A:Title: Predominance of fetal type DJH joining in young children with B precursor lymphoma  
A:Reference number: PH1302; MUID:93094761  
A:Accession: PH1310  
A:Molecule type: DNA  
A:Residues: 1-15 <WAS>  
C:Keywords: heterotetramer; immunoglobulin

Query Match 42.9%; Score 15; DB 2; Length 15;  
Best Local Similarity 60.0%; Pred. No. 2.9e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 TQDDL 6  
| | |  
Db 1 TQDEL 5

Search completed: June 30, 2000, 14:54:15  
Job time: 5180 sec

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OM protein - protein search, using sw model

Run on: June 30, 2000, 14:52:37 ; Search time 39.08 Seconds

(without alignments)  
5.455 Million cell updates/sec

Title: US-08-833-506c-89

Perfect score: 35

Sequence: 1 VTQDDIQ 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 83857 seqs, 30454973 residues

Total number of hits satisfying chosen parameters: 668

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Listing first 100 summaries

Database : SwissProt\_38.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	57.1	15	PSAO_CUCSA	P42052 cucumis sat
2	17	48.6	5	BIOA_CITFR	P13071 citrobacter
3	17	48.6	5	BIOA_SALTY	P12677 salmoneilla
4	17	48.6	9	UF02_MOUSE	P38640 mus musculus
5	16	45.7	12	XYLA_STRVN	P14405 streptomyce
6	16	45.7	14	YGBH_TREAC	Q05213 thermoplasm
7	15	42.9	11	UF05_MOUSE	P38643 mus musculus
8	15	42.9	13	ACT7_SOYBN	P15987 glycine max
9	15	42.9	14	GLGS_SPIOL	P55235 spinacia ol
10	14	40.0	10	UXA7_CHLTR	P38008 chlamydia t
11	14	40.0	11	T2P1_PROVU	P31031 proteus vul
12	14	40.0	12	UP01_CAEEL	P55954 caenorhabdi
13	14	40.0	13	UN02_PINPS	P81667 pinus pinas
14	14	40.0	14	RECU_SALTY	P28355 salmoneilla
15	14	40.0	15	FRB7_PINPS	P81104 pinus pinas
16	13	37.1	11	FAR9_CALVO	P41864 calliphora
17	13	37.1	12	LOSK_LOEMI	P47733 locusta mig
18	13	37.1	12	ULAL_MOUSE	P99032 mus musculus
19	13	37.1	13	EP65_HUMAN	P54963 homo sapien
20	13	37.1	13	LIGA_TRAVE	P20011 trameetes ve
21	13	37.1	13	LIGB_TRAVE	P20012 trameetes ve
22	13	37.1	13	RL30_SALTY	O54300 salmoneilla
23	13	37.1	14	HCYA_MEGCR	Q10583 megathura c
24	13	37.1	15	ITRB_ALBUU	P24927 albizzia ju
25	13	37.1	15	RKGG_CARCR	P21586 caretta car
26	13	37.1	15	UN01_PINPS	P81106 pinus pinas
27	12	34.3	9	FAR2_CALVO	P41857 calliphora
28	12	34.3	9	FAR3_CALVO	P41858 calliphora
29	12	34.3	9	NSK1_SARBU	P41492 sarcophaga
30	12	34.3	9	UHA2_HUMAN	P40929 homo sapien
31	12	34.3	9	ULAH_HUMAN	P31934 homo sapien
32	12	34.3	10	FARC_CALVO	P41867 calliphora
33	12	34.3	10	FIBB_CERSI	P14537 ceratotheri
34	12	34.3	10	GS09_BACSU	P80243 bacillus su

35	12	34.3	10	LSK2_LEUMA	P09039 leucophaea
36	12	34.3	10	UPA2_HUMAN	P30088 homo sapien
37	12	34.3	11	LSRP_PERAM	P36885 periplaneta
38	12	34.3	11	RR2_CONAM	P42341 conopholis
39	12	34.3	11	RRPL_CHAV	P13179 chandipura
40	12	34.3	12	CALM_TETTH	Q05055 tetrahymena
41	12	34.3	13	FIBB_RABIT	P14478 oryctolagus
42	12	34.3	13	ODPA_CANFA	P49823 canis famill
43	12	34.3	13	UN10_CLOPA	P81345 clostridium
44	12	34.3	14	LECB_PSOSC	P29399 psophocarpu
45	12	34.3	14	MARI_ALTSP	P29399 alteromonas
46	12	34.3	14	NSK2_SARBU	P41493 sarcophaga
47	12	34.3	14	TKNM_RANNA	P40951 rana margar
48	12	34.3	15	48KD_BACCE	P80173 bacillus ce
49	12	34.3	15	UC28_WAIZE	P80634 zea mays (m
50	11	31.4	8	CLP_THICU	P80488 thlobacillu
51	11	31.4	9	DI_NEPNO	P24816 nephrops no
52	11	31.4	9	DCML_PSECF	P19913 pseudomonas
53	11	31.4	9	FAR1_CALVO	P41856 calliphora
54	11	31.4	9	FAR4_CALVO	P41859 calliphora
55	11	31.4	9	FAR5_CALVO	P41860 calliphora
56	11	31.4	9	FAR6_CALVO	P41861 calliphora
57	11	31.4	9	FAR7_CALVO	P41862 calliphora
58	11	31.4	9	FARD_CALVO	P41868 calliphora
59	11	31.4	9	LMTP_LOEMI	P31799 locusta mig
60	11	31.4	10	CAER_LITXA	P56264 litoria xan
61	11	31.4	10	FARP_WANSE	P18523 manduca sex
62	11	31.4	10	LCMS_LEUMA	P21144 leucophaea
63	11	31.4	10	SPI_HALRO	Q10997 halocynthia
64	11	31.4	10	UH05_RAT	P56573 rattus norv
65	11	31.4	10	XVNB_DICBA	P80717 dictyoglomu
66	11	31.4	13	GER1_HORVU	P28525 hordeum vul
67	11	31.4	13	GER2_HORVU	P28526 hordeum vul
68	11	31.4	13	PSAJ_PEA	P17229 pisum sativ
69	11	31.4	14	LPW_RHIME	P18854 rhizobium m
70	11	31.4	14	UN46_CLOPA	P81362 clostridium
71	11	31.4	15	CYSK_CLOPA	P81340 clostridium
72	11	31.4	15	FIBA_ANAPL	P12801 andas piatyr
73	11	31.4	15	MAOX_CHICK	Q92060 gallus gall
74	11	31.4	15	PKKH_PHYPA	P80659 physcomitre
75	11	31.4	15	PGTS_PELAC	P80564 pelobacter
76	11	31.4	15	TERM_BPM2	P19897 bacterioph
77	10	28.6	6	TRPI_PSEPU	P36414 pseudomonas
78	10	28.6	9	FIBB_PAPAN	P19344 papio anubi
79	10	28.6	9	FIBB_PAPHA	P19343 papio hamad
80	10	28.6	9	FIBB_THEGE	P19342 theropithe
81	10	28.6	10	COXA_ONCMY	P80328 oncorhynch
82	10	28.6	10	MALE_KLEPN	Q05564 klebsiella
83	10	28.6	10	MOSQ_CLYXA	P19962 clypeaster
84	10	28.6	11	TKN1_OPERU	P08612 uperoleia r
85	10	28.6	12	HCYB_MEGCR	Q10584 megathura c
86	10	28.6	12	TKN_KASSE	P08611 kassina sen
87	10	28.6	12	UCRH_MOUSE	P99028 mus musculus
88	10	28.6	12	UR2_GILMI	P01147 gillichthys
89	10	28.6	13	ECDE_LYMDI	P80941 lymantria d
90	10	28.6	13	IDHC_FIG	P20304 sus scrofa
91	10	28.6	13	LPAA_PORGI	P81411 porphyromon
92	10	28.6	13	ORCK_ORCLI	P37086 orconectes
93	10	28.6	13	PRC_SALTY	P43669 salmoneilla
94	10	28.6	13	SODM_CANFA	P54712 canis famill
95	10	28.6	13	UHA1_HUMAN	P40928 homo sapien
96	10	28.6	13	UN12_CLOPA	P81353 clostridium
97	10	28.6	14	ALYT_ALYOC	P08944 alytes obst
98	10	28.6	14	DHSL_ANACY	P17874 anabaena cy
99	10	28.6	14	GR75_CANFA	P99502 canis famill
100	10	28.6	14	SODN_STRCO	P80735 streptomyce

#### ALIGNMENTS

RESULT 1  
PSNO\_CUCSA

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ID PSNO_CUCSA STANDARD; PRT; 15 AA.
AC P42052;
DT 01-NOV-1995 (Rel. 32, Last Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE PHOTOSYSTEM 1 REACTION CENTRE SUBUNIT 8 (PHOTOSYSTEM I 17.5 KD
DE PROTEIN) (FRAGMENT).
GN PSAM.
OS Cucumis sativus (Cucumber).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Rosidae; eurosids I; Cucurbitales; Cucurbitaceae;
OC Cucumis.
RN [1]
RP SEQUENCE.
RC TISSUE-COTYLEDON;
RX MEDLINE; 91355209.
RA Iwasaki Y., Ishikawa H., Hibino T., Takabe T.;
RT "Characterization of genes that encode subunits of cucumber PS I
RT complex by N-terminal sequencing."
RL Biochim. Biophys. Acta 1059:141-148(1991).
CC -1- FUNCTION: ESSENTIAL FOR THE ACTIVITY OF NADP PHOTOREDUCTION.
KW Photosystem I; Photosynthesis; Chloroplast; Thylakoid membrane.
FT NON_TER 15
SQ SEQUENCE 15 AA; 1714 MW; CA0BF5DAD403D9F4 CRC64;

Query Match 57.1%; Score 20; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VTQDD 5
DB 10 VIQDD 14

RESULT 2
BIOA_CITFR STANDARD; PRT; 5 AA.
ID BIOA_CITFR STANDARD; PRT; 5 AA.
AC P13071;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE ADENOSYLMETHIONINE-8-AMINO-7-OXONONANOATE AMINOTRANSFERASE
DE (EC 2.6.1.62) (7,8-DIAMINO-PELARGONIC ACID AMINOTRANSFERASE) (DAPA
DE AMINOTRANSFERASE) (FRAGMENT).
GN BIOA.
OS Citrobacter freundii.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Citrobacter.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89006280.
RA Shuan D., Campbell A.;
RT "Transcriptional regulation and gene arrangement of Escherichia coli,
RT Citrobacter freundii and Salmonella typhimurium biotin operons.";
RL Gene 67:203-211(1988).
CC -1- CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE + 8-AMINO-7-
CC OXONONANOATE -> S-ADENOSYL-4-METHYLTHIO-2-OXOBUTANOATE +
CC 7,8-DIAMINONONANOATE.
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -1- PATHWAY: BIOTIN BIOSYNTHESIS.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SIMILARITY: BELONGS TO CLASS-III OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC AMINOTRANSFERASES.
CC
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CC
CC EMBL; M21923; CAB25181.1; -
CC STYGENE; SG10026; BIOA.
DR PROSITE; PS00600; AA_TRANSFER_CLASS_3; PARTIAL.
KW Biotin biosynthesis; Transferase; Aminotransferase;
FT Pyridoxal phosphate. 5
FT NON_TER 5
SQ SEQUENCE 5 AA; 582 MW; 6AAAB1B1A6F00000 CRC64;

Query Match 48.6%; Score 17; DB 1; Length 5;
Best Local Similarity 60.0%; Pred. No. 8.4e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VTQDD 5
DB 1 MTQDD 5

RESULT 3
BIOA_SALTY STANDARD; PRT; 5 AA.
ID BIOA_SALTY STANDARD; PRT; 5 AA.
AC P12677;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE ADENOSYLMETHIONINE-8-AMINO-7-OXONONANOATE AMINOTRANSFERASE
DE (EC 2.6.1.62) (7,8-DIAMINO-PELARGONIC ACID AMINOTRANSFERASE) (DAPA
DE AMINOTRANSFERASE) (FRAGMENT).
GN BIOA.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC OC Salmonella.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89006280.
RA Shuan D., Campbell A.;
RT "Transcriptional regulation and gene arrangement of Escherichia coli,
RT Citrobacter freundii and Salmonella typhimurium biotin operons.";
RL Gene 67:203-211(1988).
CC -1- CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE + 8-AMINO-7-
CC OXONONANOATE -> S-ADENOSYL-4-METHYLTHIO-2-OXOBUTANOATE +
CC 7,8-DIAMINONONANOATE.
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -1- PATHWAY: BIOTIN BIOSYNTHESIS.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SIMILARITY: BELONGS TO CLASS-III OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC AMINOTRANSFERASES.
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M21923; CAB25181.1; -
CC STYGENE; SG10026; BIOA.
DR PROSITE; PS00600; AA_TRANSFER_CLASS_3; PARTIAL.
KW Biotin biosynthesis; Transferase; Aminotransferase;
FT Pyridoxal phosphate. 5
FT NON_TER 5
SQ SEQUENCE 5 AA; 582 MW; 6AAAB1B1A6F00000 CRC64;

Query Match 48.6%; Score 17; DB 1; Length 5;
Best Local Similarity 60.0%; Pred. No. 8.4e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VTQDD 5
DB 1 MTQDD 5
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```
RESULT 4
UF02_MOUSE STANDARD; PRT; 9 AA.
ID P38640;
AC DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE UNKNOWN PROTEIN FROM 2D-PAGE OF FIBROBLASTS (P32) (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE.
RC TISSUE=FIBROBLAST;
RX MEDLINE; 95009907.
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins
RT using preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.0, ITS MW IS: 32 KD.
FT NON_TER 9
FT SEQUENCE 9 AA; 1102 MW; 7E73EAB6D05B1AAB CRC64;

Query Match 48.6%; Score 17; DB 1; Length 9;
Best Local Similarity 40.0%; Pred. No. 8.4e+04;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 QDDIQ 7
DB 2 EDEIQ 6

RESULT 5
XYLA_STRVN STANDARD; PRT; 12 AA.
ID P14405;
AC DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE XYLOSE ISOMERASE (EC 5.3.1.5) (FRAGMENT).
OS Streptomyces violaceoruber.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
RN [1]
RP SEQUENCE.
RC STRAIN=LMG 7183;
RX MEDLINE; 90104230.
RA Vangrypsperre W., Ampe C., Kersters-Hilderson H., Tempst P.;
RT "Single active-site histidine in D-xylose isomerase from Streptomyces
RT violaceoruber. Identification by chemical derivatization and peptide
RT mapping.";
RL Biochem. J. 263:195-199(1989).
CC -1- CATALYTIC ACTIVITY: D-XYLOSE -> D-XYLULOSE.
CC -1- COFACTOR: MAGNESIUM IS NECESSARY FOR THE ACTIVITY.
CC -1- SUBUNIT: HOMOTETRAMER.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE XYLOSE ISOMERASE FAMILY.
DR HSSP: P37031; 1DXI.
DR PROSITE: PS00172; XYLOSE ISOMERASE_1; PARTIAL.
DR PROSITE: PS00173; XYLOSE ISOMERASE_2; PARTIAL.
KW Isomerase; Pentose shunt; Xylose metabolism; Magnesium.
FT NON_TER 1
FT ACT_SITE 5
FT NON_TER 12
FT SEQUENCE 12 AA; 1375 MW; E749268EBIAAAAAA1 CRC64;

Query Match 45.7%; Score 16; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 4 DDL 6
DB 7 DDL 9

RESULT 6
YGDH_THEAC STANDARD; PRT; 14 AA.
ID Q05213;
AC DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE HYPOTHETICAL PROTEIN IN GLUCOSE DEHYDROGENASE GENE 3'REGION
DE (FRAGMENT).
OS Thermoplasma acidophilum.
OC Archaea; Euryarchaeota; Thermoplasmatales; Thermoplasmaceae;
OC Thermoplasma.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 1728;
RX MEDLINE; 93170285.
RA Bright J.R., Byrom D., Danson M.J., Hough D.W., Towner P.;
RT "Cloning, sequencing and expression of the gene encoding glucose
RT dehydrogenase from the thermophilic archaeon Thermoplasma
RT acidophilum.";
RL Eur. J. Biochem. 211:549-554(1993).
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X59788; CAA42451.1; -
DR PIR; S29789; S29789.
KW Hypothetical protein.
FT NON_TER 14
FT SEQUENCE 14 AA; 1674 MW; 685A1FFF26529944 CRC64;

Query Match 45.7%; Score 16; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDL 6
DB 9 DDL 11

RESULT 7
UF05_MOUSE STANDARD; PRT; 11 AA.
ID P38643;
AC DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE UNKNOWN PROTEIN FROM 2D-PAGE OF FIBROBLASTS (P48) (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE.
RC TISSUE=FIBROBLAST;
RX MEDLINE; 95009907.
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins
RT using preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.5, ITS MW IS: 48 KD.
```

```
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1328 MW; E54835E5CAABAF6A CRC64;

Query Match 42.9%; Score 15; DB 1; Length 11;
Best Local Similarity 33.3%; Pred. No. 9.7e+02;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VTQDL 6
   : ||:
Db 3 IXXDV 8

RESULT 8
ACT7_SOYBN STANDARD; PRT; 13 AA.
AC P15987:
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DE 13-JUL-1999 (Rel. 38, Last annotation update)
DE ACTIN 7 (FRAGMENT).
GN SAC7.
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC eukaryotes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae;
OC Glycine.
RN [1]
RP SEQUENCE FROM N. A.
RC STRAIN-CV WAYNE;
RX MEDLINE; 91346640.
RA Pearson L., Meagher R.B.;
RT "Diverse soybean actin transcripts contain a large intron in the 5',
RT untranslated leader: structural similarity to vertebrate muscle actin
RT genes.";
RL Plant Mol. Biol. 14:513-526(1990).
CC -1- FUNCTION: ACTINS ARE HIGHLY CONSERVED PROTEINS THAT ARE INVOLVED
CC IN VARIOUS TYPES OF CELL MOTILITY AND ARE UBIQUITOUSLY EXPRESSED
CC IN ALL EUKARYOTIC CELLS.
CC -1- FUNCTION: ESSENTIAL COMPONENT OF CELL CYTOSKELETON; PLAYS AN
CC IMPORTANT ROLE IN CYTOPLASMIC STREAMING, CELL SHAPE DETERMINATION,
CC CELL DIVISION, ORGANELLE MOVEMENT AND EXTENSION GROWTH.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- MISCELLANEOUS: THERE ARE AT LEAST 16 ACTIN GENES IN SOYBEAN.
CC -1- SIMILARITY: BELONGS TO THE ACTIN FAMILY.
-----
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DR EMBL: X17120; CAA34980.1; -.
DR PIR: S15755; S15755.
DR PROSITE; PS00406; ACTINS.1; PARTIAL.
DR PROSITE; PS00432; ACTINS.2; PARTIAL.
DR PROSITE; PS01132; ACTINS.ACT-LIKE; PARTIAL.
KW Structural protein; Multigene family.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1420 MW; 8BEFF3C6D4FD05A CRC64;

Query Match 42.9%; Score 15; DB 1; Length 13;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DDLQ 7
   : ||:
Db 5 EDIQ 8

us-08-833-506c-89.shoert.rsp
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RESULT 9
GLGS_SPIOL STANDARD; PRT; 14 AA.
AC P55235:
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE GLUCOSE-1-PHOSPHATE ADENYLYLTRANSFERASE SMALL SUBUNIT (EC 2.7.7.27)
DE (ADP-GLUCOSE SYNTHASE) (ADP-GLUCOSE PYROPHOSPHORYLASE) (AGPASE B)
DE (ALPHA-D-GLUCOSE-1-PHOSPHATE ADENYL TRANSFERASE) (FRAGMENT).
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC eukaryotes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Caryophyllales; Caryophyllales; Chenopodiaceae;
OC Spinacia.
RN [1]
RP SEQUENCE.
RC TISSUE-LEAF;
RA Morell M.K., Bloom M., Knowles V., Preiss J.;
RT "Subunit structure of spinach leaf ADPglucose pyrophosphorylase.";
RL Plant Physiol. 85:182-187(1987).
CC -1- FUNCTION: THIS PROTEIN PLAYS A ROLE IN SYNTHESIS OF STARCH.
CC IT CATALYSES THE SYNTHESIS OF THE ACTIVATED GLYCOSYL DONOR,
CC ADP-GLUCOSE FROM GLC-1-P AND ATP.
CC -1- CATALYTIC ACTIVITY: ATP + ALPHA-D-GLUCOSE 1-PHOSPHATE =
CC PYROPHOSPHATE + ADP-GLUCOSE.
CC -1- ENZYME REGULATION: ACTIVATED BY 3'PHOSPHOGLYCERATE, INHIBITED
CC BY ORTHOPHOSPHATE. ALLOSTERIC REGULATION.
CC -1- PATHWAY: STARCH BIOSYNTHESIS.
CC -1- SUBUNIT: HETEROTETRAMER.
CC -1- SUBCELLULAR LOCATION: CHLOROPLASTS OF LEAVES AND AMYLOPLASTS
CC OF DEVELOPING ENDOSPERM.
CC -1- SIMILARITY: BELONGS TO THE BACTERIAL AND PLANTS GLUCOSE-1-
CC PHOSPHATE ADENYLYLTRANSFERASE FAMILY.
DR PROSITE; PS00808; ADP_GLC_PYROPHOSPH_1; PARTIAL.
DR PROSITE; PS00809; ADP_GLC_PYROPHOSPH_2; PARTIAL.
DR PROSITE; PS00810; ADP_GLC_PYROPHOSPH_3; PARTIAL.
KW Glycogen biosynthesis; Transferase; Nucleotidyltransferase;
KW Multigene family; Starch biosynthesis; Allosteric enzyme;
KW Amyloplast; Chloroplast.
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1490 MW; 98B5792C3AE738C5 CRC64;

Query Match 42.9%; Score 15; DB 1; Length 14;
Best Local Similarity 60.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TQDDL 6
   : ||:
Db 7 SQDGL 11

us-08-833-506c-89.shoert.rsp
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RESULT 10
UXAV_CHLTR STANDARD; PRT; 10 AA.
AC P38008:
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE UNKNOWN PROTEIN FROM 2D-PAGE FROM ELEMENTARY BODY (FRAGMENT).
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
RN [1]
RP SEQUENCE.
RC STRAIN=L2/434/BU;
RA Bini L., Santucci A., Magl B., Marzocchi B., Sanchez-Campillo M.,
RA Comanducci M., Christianen G., Birkelund S., Vretou E., Ratti G.,
RA Pallini V.;
RL Submitted (SEP-1994) to the SWISS-PROT data bank.
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.65 OR 6.89 (TWO SPOTS ARE PRESENT), ITS MW IS: 70
CC KD.
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FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1251 MW; 80A43FD6D731AAB1 CRC64;

Query Match
Best Local Similarity 40.0%; Score 14; DB 1; Length 10;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 DDLQ 7
DB 4 DTLQ 7

RESULT 11
T2PL_PROVU STANDARD; PRT; 11 AA.
AC P31031;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE TYPE II RESTRICTION ENZYME PVUI (EC 3.1.21.4) (ENDONUCLEASE PVUI)
DE (R. PVUI) (FRAGMENT).
OS Proteus vulgaris.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Proteus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 13315;
RX MEDLINE; 93087186.
RA Smith M.D., Longo M., Gerard G.F., Chatterjee D.K.;
RT "Cloning and characterization of genes for the Pvui restriction and
modification system.";
RL Nucleic Acids Res 20:5743-5747(1992).
CC -!- CATALYTIC ACTIVITY: RECOGNIZES THE DOUBLE-STRANDED SEQUENCE CGATCG
CC AND CLEAVES AFTER T-4.
CC -----
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CC -----
DR EMBL; L04163; AAA25660.1; -
DR PIR; S35490; S35490.
DR REBASE; RB00107; Pvui.
KW Hydrolase; Endonuclease; Nuclease; Restriction system.
FT NON_TER 1
SQ SEQUENCE 11 AA; 1300 MW; 9F0CDE7955B72B1A CRC64;

Query Match
Best Local Similarity 40.0%; Score 14; DB 1; Length 11;
Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 VTODDL 6
DB 1 ISVDEL 6

RESULT 12
UP01_CAEEL STANDARD; PRT; 12 AA.
AC P55954;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE UNKNOWN PROTEIN FROM 2D-PAGE (SPOT 1) (FRAGMENT).
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;
OC Rhabditina; Rhabditidae; Rhabditidae; Peloderinae; Caenorhabditis.
RN [1]
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RP SEQUENCE.
RC STRAIN-BRISTOL N2;
RX MEDLINE; 97295299.
RA Bini L., Heid H., Liberatori S., Geier G., Pallini V., Zwilling R.;
RT "Two-dimensional gel electrophoresis of Caenorhabditis elegans
homogenates and identification of protein spots by microsequencing.";
RL Electrophoresis 18:557-562(1997).
FT NON_TER 12
SQ SEQUENCE 12 AA; 1409 MW; 8DC4A7105316905A CRC64;

Query Match
Best Local Similarity 40.0%; Score 14; DB 1; Length 12;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDL 6
DB 4 DDI 6

RESULT 13
UN02_PINPS STANDARD; PRT; 13 AA.
ID UN02_PINPS
AC P81667;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE UNKNOWN PROTEIN FROM 2D-PAGE OF NEEDLES (N55) (FRAGMENTS).
OS Pinus pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Coniferopsida; Coniferales; Pinaceae;
OC Pinus.
RN [1]
RP SEQUENCE.
RC TISSUE-NEEDLE;
RX MEDLINE; 99274088.
RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
RA Frigerio J.-M., Plomion C.;
RT "Separation and characterization of needle and xylem maritime pine
proteins.";
RL Electrophoresis 20:1098-1108(1999).
CC -!- INDUCTION: BY WATER-STRESS.
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.4, ITS MW IS: 43 KD.
FT NON_TER 1
FT NON_CONS 7
FT NON_TER 13
SQ SEQUENCE 13 AA; 1559 MW; 966B5A43EF94B411 CRC64;

Query Match
Best Local Similarity 40.0%; Score 14; DB 1; Length 13;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 TODDL 6
DB 6 TRDNV 10

RESULT 14
RECJ_SALTY STANDARD; PRT; 14 AA.
ID RECJ_SALTY
AC P28355;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE SINGLE-STRANDED-DNA-SPECIFIC EXONUCLEASE RECJ (EC 3.1.-.-) (FRAGMENT).
GN RECJ.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
RN [1]
RP SEQUENCE FROM N.A.
```

RX MEDLINE; 91046011.  
RA Kawakami K., Nakamura Y.;  
RT "Autogenous suppression of an opal mutation in the gene encoding  
RL Peptide chain release factor 2.";  
RL Proc. Natl. Acad. Sci. U.S.A. 87:8432-8436(1990).  
CC -1- FUNCTION: SINGLE-STRANDED-DNA-SPECIFIC EXONUCLEASE. REQUIRED FOR  
CC MANY TYPES OF RECOMBINATIONAL EVENTS, ALTHOUGH THE STRINGENCY OF  
CC THE REQUIREMENT FOR RECJ APPEARS TO VARY WITH THE TYPE OF  
CC RECOMBINATIONAL EVENT MONITORED AND THE OTHER RECOMBINATION GENE  
CC PRODUCTS WHICH ARE AVAILABLE.  
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CC -----  
DR ENBL; M38590; AAA72913.1; -.  
DR STYGENE; SG10332; RECJ.  
KW Hydrolase; Nuclease; Exonuclease.  
FT NON\_TER 1  
SQ SEQUENCE 14 AA; 1696 MW; 105E784AC26C5650 CRC64;  
  
Query Match 40.0%; Score 14; DB 1; Length 14;  
Best Local Similarity 66.7%; Pred. No. 2e+03;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 4 DDL 6  
Db 9 DDI 11  
  
RESULT 15  
FKB7\_PINPS STANDARD; PRT; 15 AA.  
AC P01104;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE 70 KD PEPTIDYLPROLYL ISOMERASE (EC 5.2.1.8) (PEPTIDYLPROLYL CIS-TRANS  
DE ISOMERASE) (CYCLOPHILIN) (PIASE) (S1205-06) (FRAGMENT).  
OS Pinus pinaster (Maritime pine).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC euphyllophytes; Spermatophyta; Coniferopsida; Coniferales; Pinaceae;  
OC Pinus.  
RN [1]  
RP SEQUENCE.  
RC TISSUE=NEEDLE;  
RA Plomion C., Costa P., Bahrman N., Frigerio J.-M.;  
RT "Genetic analysis of needle proteins in maritime pine. 1. Mapping  
RT dominant and codominant protein markers assayed on diploid tissue, in  
RT a haploid-based genetic map.";  
RL Silvae Genetica 46:161-165(1997).  
RN [2]  
RP SEQUENCE.  
RC TISSUE=NEEDLE;  
RX MEDLINE; 99274088.  
RA Costa P., Plomion C., Bauw G., Dubos C., Bahrman N., Kremer A.,  
RA Frigerio J.-M., Plomion C.;  
RT "Separation and characterization of needle and xylem maritime pine  
RT proteins.";  
RL Electrophoresis 20:1098-1108(1999).  
CC -1- FUNCTION: PPIASE THAT BINDS CALMODULIN (BY SIMILARITY).  
CC -1- CATALYTIC ACTIVITY: PEPTIDYLPROLINE (OMEGA-180) -  
CC PEPTIDYLPROLINE (OMEGA-0).  
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN IS:  
CC 5.3, ITS MW IS: 72 KD.  
CC -1- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY.  
DR PROSITE; PS00453; FKBP\_PPIASE\_1; PARTIAL.  
DR PROSITE; PS00454; FKBP\_PPIASE\_2; PARTIAL.

DR PROSITE; PS00509; FKBP\_PPIASE\_3; PARTIAL.  
KW Isomerase; Rotamase; Repeat; Calmodulin-binding.  
FT NON\_TER 1  
FT NON\_TER 15  
SQ SEQUENCE 15 AA; 1675 MW; 2B53999722277F3F CRC64;  
  
Query Match 40.0%; Score 14; DB 1; Length 15;  
Best Local Similarity 33.3%; Pred. No. 2.2e+03;  
Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2 TQDDLQ 7  
Db 10 TGDEVE 15  
  
RESULT 16  
FAR9\_CALVO STANDARD; PRT; 11 AA.  
ID FAR9\_CALVO  
AC P41864;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE CALLIFERFAMIDE 9.  
OS Calliphora vomitoria (Blue blowfly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Oestroidea; Calliphoridae; Calliphora.  
RN [1]  
RP SEQUENCE.  
RC TISSUE=THORACIC GANGLION;  
RX MEDLINE; 92196111.  
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,  
RA Rehfeld J.F., Thorpe A.;  
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2  
RT neuropeptides (designated callifMFamides) from the blowfly  
RT Calliphora vomitoria.";  
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).  
CC -1- SIMILARITY: BELONGS TO THE FARP (PMRFAMIDE RELATED PEPTIDE)  
CC FAMILY.  
DR PIR; I41978; I41978.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 11  
FT SEQUENCE 11 AA; 1359 MW; 8160CE46CAA44321 CRC64;  
  
Query Match 37.1%; Score 13; DB 1; Length 11;  
Best Local Similarity 50.0%; Pred. No. 2.5e+03;  
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 TQDD 5  
Db 4 TKND 7  
  
RESULT 17  
LOSK\_LOCFMI STANDARD; PRT; 12 AA.  
ID LOSK\_LOCFMI  
AC P47733;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE SULFAKININ (LOW-SK).  
OS Locusta migratoria (Migratory locust).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Orthoptera; Orthoptera; Caelifera;  
OC Acridomorpha; Acridoidea; Acrididae; Oedipodinae; Locusta.  
RN [1]  
RP SEQUENCE.  
RC TISSUE=BRAIN;  
RA Schoofs L., Holman G.L., Hayes T.K., Nachman R.J., de Loof A.;  
RL (In) McCaffery A., Wilson I. (eds.);  
RL Chromatography and isolation of insect hormones and pheromones,

RL pp.231-241, Plenum Press, New York (1990).  
CC -!- FUNCTION: MYOTROPIC PEPTIDE.  
CC -!- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.  
DR PROSITE; PS00259; GASTRIN; 1.  
KW Hormone; Amigation; Sulfatation.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD\_RES 7 7 SULFATATION (POTENTIAL).  
FT MOD\_RES 12 12 AMIDATION.  
SQ SEQUENCE 12 AA; 1440 MW; 9B5B5DA9BD655AAA CRC64;

Query Match 37.1%; Score 13; DB 1; Length 12;  
Best Local Similarity 40.0%; Pred. No. 2.8e+03;  
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 VTQDD 5  
DB 2 LASDD 6

RESULT 18  
ID ULAL\_MOUSE STANDARD; PRT; 12 AA.  
AC P99032;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE UNKNOWN PROTEIN FROM 2D-PAGE OF LIVER TISSUE (SPOT 2D-0014M9)  
DE (FRAGMENT).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
RN [1]  
RP SEQUENCE.  
RC TISSUE=LIVER;  
RA Sanchez J.-C., Rouge V., Frutiger S., Hughes G.J., Yan J.X.,  
RA Hooiland C., Appel R.D., Binz P.-A., Hochstrasser D.F.,  
RA Cowthorne M.;  
RL Submitted (AUG-1998) to the SWISS-PROT data bank.  
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
CC PROTEIN IS: 5.0, ITS MW IS: 11.7 KD.  
DR SWISS-2DPAGE; P99032; MOUSE.  
KW NON\_TER 12 12  
FT SEQUENCE 12 AA; 1324 MW; DD6468EE9F75BAB6 CRC64;

Query Match 37.1%; Score 13; DB 1; Length 12;  
Best Local Similarity 50.0%; Pred. No. 2.8e+03;  
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDLQ 7  
DB 2 DNVQ 5

RESULT 19  
ID EP65\_HUMAN STANDARD; PRT; 13 AA.  
AC P54963;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DE ERYTHROCYTE 65 KD PROTEIN (P65) (FRAGMENT).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.  
RN [1]  
RP SEQUENCE, AND CARBOHYDRATE-BINDING SITE.  
RX MEDLINE; 90004678.  
RA Hart G.W., Haitiwanger R.S., Holt G.D., Kelly W.G.;  
RT "Nucleoplasmic and cytoplasmic glycoproteins.";  
RL Ciba Found. Symp. 145:102-118(1989).  
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.

KW Glycoprotein. 1  
FT NON\_TER 1 1  
FT CARBOHYD 2 2 O-LINKED (GLCNAC).  
FT NON\_TER 13 13  
SQ SEQUENCE 13 AA; 1300 MW; D0B873344C61A776 CRC64;  
Query Match 37.1%; Score 13; DB 1; Length 13;  
Best Local Similarity 50.0%; Pred. No. 3e+03;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 VTQDD 6  
DB 4 VSQPSL 9

RESULT 20  
ID LIGA\_TRAVE STANDARD; PRT; 13 AA.  
AC P20011;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 01-FEB-1991 (Rel. 17, Last annotation update)  
DE LIGNINASE A (EC 1.11.1.-) (LIGNIN PEROXIDASE) (FRAGMENT).  
OS Trametes versicolor (White-rot fungus).  
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Aphyllophorales;  
OC Coriolaceae; Trametes.  
RN [1]  
RP SEQUENCE.  
RX MEDLINE; 89211432.  
RA Joensson L., Karlsson O., Lundquist K., Nyman P.O.;  
RT "Trametes versicolor ligninase: isozyme sequence homology and  
RT substrate specificity";  
RL FEBS Lett. 247:143-146(1989).  
CC -!- CATALYTIC ACTIVITY: DEPOLYMERIZATION OF LIGNIN. CATALYSES THE  
CC C (ALPHA)-C (BETA) CLEAVAGE OF THE PROPYL SIDE CHAINS OF LIGNIN.  
CC -!- PATHWAY: FIRST STEP IN LIGNIN DEGRADATION.  
DR PIR; S04013; S04013.  
DR PROSITE; P500435; PEROXIDASE\_1; PARTIAL.  
DR PROSITE; P500436; PEROXIDASE\_2; PARTIAL.  
KW Oxidoreductase; Peroxidase; Heme; Glycoprotein; Multigene family;  
KW Lignin degradation.  
FT NON\_TER 13 13  
SQ SEQUENCE 13 AA; 1298 MW; 22C50ED5872A4338 CRC64;

Query Match 37.1%; Score 13; DB 1; Length 13;  
Best Local Similarity 60.0%; Pred. No. 3e+03;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 VTQDD 5  
DB 1 VTXP 5

RESULT 21  
ID LIGA\_TRAVE STANDARD; PRT; 13 AA.  
AC P20012;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 01-FEB-1991 (Rel. 17, Last annotation update)  
DE LIGNINASE B (EC 1.11.1.-) (LIGNIN PEROXIDASE) (FRAGMENT).  
OS Trametes versicolor (White-rot fungus).  
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Aphyllophorales;  
OC Coriolaceae; Trametes.  
RN [1]  
RP SEQUENCE.  
RX MEDLINE; 89211432.  
RA Joensson L., Karlsson O., Lundquist K., Nyman P.O.;  
RT "Trametes versicolor ligninase: isozyme sequence homology and  
RT substrate specificity";  
RL FEBS Lett. 247:143-146(1989).

```
CC -|- CATALYTIC ACTIVITY: DEPOLYMERIZATION OF LIGNIN. CATALYSES THE
CC -|- C(ALPHA)-C(BETA) CLEAVAGE OF THE PROPYL SIDE CHAINS OF LIGNIN.
CC PIR; S04014; S04014.
DR PROSITE; PS00435; PEROXIDASE_1; PARTIAL.
DR PROSITE; PS00436; PEROXIDASE_2; PARTIAL.
KW Oxidoreductase; Peroxidase; Heme; Glycoprotein; Multigene family;
KW Lignin degradation. 13
FT NON_TER 13
SQ SEQUENCE 13 AA; 1269 MW; 22C50ED5872A52C8 CRC64;

Query Match 37.1%; Score 13; DB 1; Length 13;
Best Local Similarity 60.0%; Pred. No. 3e+03;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VTQDD 5
Db 1 VTXP 5

RESULT 22
RL30_SALTY STANDARD; PRT; 13 AA.
AC O54300;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE 50S RIBOSOMAL PROTEIN L30 (FRAGMENT).
GN RPNM.
OS Salmonella typhimurium.
CC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
CC Salmonella.
CC [1]
RP SEQUENCE FROM N.A.
RA Bjorkman J., Hughes D., Andersson D.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
CC -|- SIMILARITY: BELONGS TO THE L30P FAMILY OF RIBOSOMAL PROTEINS.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
DR EMBL: AJ223237; CAAL1206.1; -
DR STYGENE; SG7777; RPNM.
DR PROSITE; PS00634; RIBOSOMAL_L30; PARTIAL.
KW Ribosomal protein.
FT INIT_MET 0 BY SIMILARITY.
FT NON_TER 13
SQ SEQUENCE 13 AA; 1431 MW; 15A0A8F8E6B3C1A0 CRC64;

Query Match 37.1%; Score 13; DB 1; Length 13;
Best Local Similarity 66.7%; Pred. No. 3e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VTQ 3
Db 6 ITQ 8

RESULT 23
HCYA_MEGCR STANDARD; PRT; 14 AA.
AC Q10583;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
```

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DE HEMOCYANIN A CHAIN (KLH-A) (FRAGMENT).
OS Megathura crenulata.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Archaeogastropoda;
OC Patellicidae; Megathura.
RN [1]
RP SEQUENCE.
RX MEDLINE; 96208935.
RA Swerdlow R.D., Ebert R.F., Lee P., Bonaventura C., Miller K.I.;
RT "Keyhole limpet hemocyanin: structural and functional
RT characterization of two different subunits and multimers.";
RL Comp. Biochem. Physiol. 113B:537-548(1996).
CC -|- FUNCTION: HEMOCYANIN ARE COPPER-CONTAINING OXYGEN CARRIERS
CC OCCURRING FREELY DISSOLVED IN THE HEMOLYMPH OF MANY MOLLUSKS AND
CC ARTHROPODS.
CC -|- SUBUNIT: DECAMERS AND DIDECAMERS.
CC -|- SUBCELLULAR LOCATION: EXTRACELLULAR.
CC -|- TISSUE SPECIFICITY: HEMOLYMPH.
CC -|- SIMILARITY: BELONGS TO THE TYROSINASE FAMILY. HEMOCYANIN
CC SUBFAMILY.
DR PROSITE; PS00209; HEMOCYANIN_1; PARTIAL.
DR PROSITE; PS00210; HEMOCYANIN_2; PARTIAL.
KW Respiratory protein; Oxygen transport; Copper; Glycoprotein;
KW Hemolymph.
FT NON_TER 14
SQ SEQUENCE 14 AA; 1610 MW; 9C61977014A99D5 CRC64;

Query Match 37.1%; Score 13; DB 1; Length 14;
Best Local Similarity 50.0%; Pred. No. 3.3e+03;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VTQD 4
Db 11 LTQE 14

RESULT 24
ITRB_ALBUJ STANDARD; PRT; 15 AA.
AC P24977;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE TRYPsin INHIBITOR B CHAIN (FRAGMENT).
OS Albizzia julibrissin (Silk tree).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Rosidae; eurosids 1; Fabales; Fabaceae; Mimosoideae;
OC Albizzia.
CC [1]
RN SEQUENCE.
RP TISSUE=SEED;
RX MEDLINE; 80115605.
RA Odani S., Ono T., Ikenaka T.;
RT "Proteinase inhibitors from a mimosoideae legume, Albizzia
RT julibrissin. Homologues of soybean trypsin inhibitor (Kunitz).";
RL J. Biochem. 86:1795-1805(1979).
CC -|- FUNCTION: INHIBITS TRYPsin AND ALPHa-CHYMOTRYPsin.
CC -|- SUBUNIT: HETERODIMER OF AN "A" AND A "B" CHAIN LINKED BY A
CC DISULFIDE BOND.
CC -|- SIMILARITY: TO BETA CHAINS OF SOME OTHER LEGUMINOUS KUNITZ-TYPE
CC INHIBITORS.
KW Serine protease inhibitor.
FT NON_TER 15
SQ SEQUENCE 15 AA; 1705 MW; 53165F7E9C45B4D0 CRC64;

Query Match 37.1%; Score 13; DB 1; Length 15;
Best Local Similarity 66.7%; Pred. No. 3.5e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ODD 5
Db 11
```

Db 1 KDD 3

RESULT 25  
ID RKG\_CARCER STANDARD; PRT; 15 AA.  
AC P21586;  
DT 01-MAY-1991 (Rel. 18, Created)  
DT 01-MAY-1991 (Rel. 18, Last sequence update)  
DT 01-MAY-1991 (Rel. 19, Last annotation update)  
DE RATHKE'S GLAND GLYCOPROTEIN (FRAGMENT).  
OS Carretta caretta (loggerhead).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Testudines;  
OC Cryptodira; Chelonioidae; Cheloniidae; Carretta.  
RN [1]  
RP SEQUENCE.  
RC TISSUE=RATHKE'S GLAND;  
RX MEDLINE; 90075703.  
RA Radhakrishna G., Chin C.C.Q., Wold F., Weldon P.J.;  
RT "Glycoproteins in Rathke's gland secretions of loggerhead (Carretta caretta) and Kemp's ridley (Lepidochelys kempi) sea turtles.";  
RL Comp. Biochem. Physiol. 94B:375-378(1989).  
CC -!- FUNCTION: RATHKE'S GLAND SECRETIONS MAY FUNCTION AS PHEROMONES, AS PREDATOR REPELLENTS, OR CONTRIBUTE TO THE MAINTENANCE OF THE TURTLE SHELL.  
CC -!- SIMILARITY: WITH RATHKE'S GLAND GLYCOPROTEIN FROM KEMP'S RIDLEY SEA TURTLE.  
CC PIR; PLO154; PLO154.  
KW Glycoprotein.  
FT NON\_TER 15 15  
SQ SEQUENCE 15 AA; 1477 MW; CC893BAAA1B1B5ED CRC64;

Query Match 37.1%; Score 13; DB 1; Length 15;  
Best Local Similarity 50.0%; Pred. No. 3.5e+03;  
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 TODD 5  
: ||  
Db 1 SDD 4

RESULT 26  
ID UNO1\_PINPS STANDARD; PRT; 15 AA.  
AC P81106;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE UNKNOWN PROTEIN FROM 2D-PAGE OF NEEDLES (S1247/S1248) (N150/N151) (FRAGMENT).  
OS Pinus pinaster (Maritime pine).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC euphyllophytes; Spermatophyta; Coniferopsida; Coniferales; Pinaceae;  
OC Pinus.  
RN [1]  
RP SEQUENCE.  
RC TISSUE=NEEDLE;  
RA Plomion C., Costa P., Bahrman N., Frigerio J.M.;  
RT "Genetic analysis of needle proteins in maritime pine. 1. Mapping dominant and codominant protein markers assayed on diploid tissue, in a haploid-based genetic map.";  
RL Silvae Genetica 46:161-165(1997).  
RN [2]  
RP SEQUENCE.  
RC TISSUE=NEEDLE;  
RX MEDLINE; 92274088.  
RA Costa P., Plomion C., Bauw G., Dubos C., Bahrman N., Kremer A., Frigerio J.-M., Plomion C.;  
RT "Separation and characterization of needle and xylem maritime pine proteins.";  
RL Electrophoresis 20:1098-1108(1999).  
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN

CC PROTEIN IS: 5.5, ITS MW IS: 62 KD.  
FT NON\_TER 1  
FT NON\_TER 15  
SQ SEQUENCE 15 AA; 1670 MW; 29CE44CD51E98FCF CRC64;

Query Match 37.1%; Score 13; DB 1; Length 15;  
Best Local Similarity 66.7%; Pred. No. 3.5e+03;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VTQ 3  
: ||  
Db 5 ITQ 7

RESULT 27  
ID FAR2\_CALVO STANDARD; PRT; 9 AA.  
AC P41857;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE CALLIFMRFAMIDE 2.  
OS Calliphora vomitoria (Blue blowfly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Oestroidea; Calliphoridae; Calliphora.  
RN [1]  
RP SEQUENCE.  
RC TISSUE=THORACIC GANGLION;  
RX MEDLINE; 92196111.  
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I., Rehfeld J.F., Thorpe A.;  
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2 neuropeptides (designated callifmrfa-mides) from the blowfly Calliphora vomitoria.";  
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).  
CC -!- FUNCTION: ABLE TO INDUCE FLUID SECRETION FROM THE ISOLATED SALIVARY GLAND OF CALLIPHORA.  
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE) FAMILY.  
CC PIR; B41978; B41978.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 9  
SQ SEQUENCE 9 AA; 1128 MW; 29D00599CAB5C5A7 CRC64;

Query Match 34.3%; Score 12; DB 1; Length 9;  
Best Local Similarity 66.7%; Pred. No. 8.4e+04;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 TOD 4  
: ||  
Db 3 SQD 5

RESULT 28  
ID FAR3\_CALVO STANDARD; PRT; 9 AA.  
AC P41858;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE CALLIFMRFAMIDE 3.  
OS Calliphora vomitoria (Blue blowfly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Oestroidea; Calliphoridae; Calliphora.  
RN [1]  
RP SEQUENCE.  
RC TISSUE=THORACIC GANGLION;  
RX MEDLINE; 92196111.  
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,

RA Rehfeld J.F., Thorpe A.;  
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2  
neuropeptides (designated callifamides) from the blowfly  
RT Calliphora vomitoria";  
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).  
CC -1- FUNCTION: ABLE TO INDUCE FLUID SECRETION FROM THE ISOLATED  
CC SALIVARY GLAND OF CALLIPHORA.  
CC -1- SIMILARITY: BELONGS TO THE FARP (FAMRFAIDE RELATED PEPTIDE)  
CC FAMILY.  
DR PIR; C41978; C41978.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 9  
SQ SEQUENCE 9 AA; 1114 MW; 2F0B0699CAB6C5A7 CRC64;

Query Match 34.3%; Score 12; DB 1; Length 9;  
Best Local Similarity 66.7%; Pred. No. 8.4e+04;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 TOP 4  
Db :||  
3 SQD 5

RESULT 29  
NSK1\_SARBU STANDARD; PRT; 9 AA.  
AC P41492;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-FEB-1996 (Rel. 33, Last annotation update)  
DE NEOSULFAKININ-I (NEB-SK-I).  
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Oestroidea; Sarcophagidae; Sarcophaga.  
RN [1]  
RP SEQUENCE.  
RC TISSUE-HEAD;  
RX MEDLINE; 93083101.  
RA Fonagy A., Schoofs L., Proost P., van Damme J., de Loof A.;  
RT "Isolation and primary structure of two sulfakinin-like peptides from  
RT the fleshfly, Neobellieria bullata";  
RL Comp. Biochem. Physiol. 103C:135-142(1992).  
CC -1- FUNCTION: MOTROPIC PEPTIDE.  
CC -1- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.  
DR PROSITE; PS00259; GASTRIN; 1.  
KW Neuropeptide; Amidation; Sulfatation.  
FT MOD\_RES 4  
FT MOD\_RES 9  
SQ SEQUENCE 9 AA; 1187 MW; 8B0A0691E86B5AAA CRC64;

Query Match 34.3%; Score 12; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 8.4e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DD 5  
Db :||  
2 DD 3

RESULT 30  
UHA2\_HUMAN STANDARD; PRT; 9 AA.  
ID P40929;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 01-FEB-1995 (Rel. 31, Last annotation update)  
DE UNKNOWN PROTEIN FROM 2D-PAGE OF HEART (SPOT 5603) (FRAGMENT).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.

RN [1]  
RP SEQUENCE.  
RC TISSUE=HEART;  
RX MEDLINE; 95203287.  
RA Corbett J.M., Wheeler C.H., Baker C.S., Yacoub M.H., Dunn M.J.;  
RT "The human myocardial two-dimensional gel protein database: update  
RT 1994.";  
RL Electrophoresis 15:1459-1465(1994).  
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
CC PROTEIN IS: 6.0, ITS MW IS: 55.3 KD.  
FT NON\_TER 9  
SQ SEQUENCE 9 AA; 1104 MW; 8874B1BB5B01B2CA CRC64;

Query Match 34.3%; Score 12; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 8.4e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DD 5  
Db :||  
8 DD 9

Search completed: June 30, 2000, 19:03:14  
Job time: 15037 sec





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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: June 30, 2000, 14:07:09 ; Search time 53.11 Seconds  
(without alignments)

9.138 Million cell updates/sec

Title: US-08-833-506C-89  
Perfect score: 35  
Sequence: 1 VTQDDIQ 7

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 225878 seqs, 69334122 residues

Total number of hits satisfying chosen parameters: 1120

Minimum DB seq length: 0  
Maximum DB seq length: 15

Post-processing: Minimum Match 0%  
Listing first 100 summaries

Database : SPTREMBL12.\*  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phage.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	57.1	12	4	Q13695 homo sapien
2	20	57.1	14	12	Q84179 porcine ade
3	19	54.3	11	9	Q38415 bacteriophage
4	17	48.6	12	8	P92457 ephedra sp.
5	17	48.6	15	2	Q53541 bacillus sp
6	15	42.9	8	4	Q15893 homo sapien
7	15	42.9	9	11	Q63924 mus musculus
8	15	42.9	11	2	Q47602 escherichia
9	15	42.9	14	11	Q921H4 mus musculus
10	15	42.9	15	4	Q08947 homo sapien
11	15	42.9	15	4	Q16387 homo sapien
12	14	40.0	8	2	P72279 rhodococcus
13	14	40.0	8	4	Q15902 homo sapien
14	14	40.0	8	5	Q94895 physarum po
15	14	40.0	11	5	Q23876 dictyostel
16	14	40.0	13	2	Q48357 escherichia
17	14	40.0	13	5	Q61340 panulirus i
18	14	40.0	14	4	Q16118 homo sapien
19	14	40.0	14	12	P91578 choristoneu
20	14	40.0	15	2	O52640 pseudomonas

21	13	37.1	9	2	Q47556	Q47556 escherichia
22	13	37.1	9	12	Q83622	Q83622 murray vall
23	13	37.1	10	11	Q83056	Q83056 rattus norv
24	13	37.1	11	4	Q16427	Q16427 homo sapien
25	13	37.1	11	7	Q78119	Q78119 oreochromis
26	13	37.1	12	8	Q36622	Q36622 picea abies
27	13	37.1	12	8	Q36623	Q36623 picea abies
28	13	37.1	12	8	Q36668	Q36668 pinus sylve
29	13	37.1	12	8	Q36669	Q36669 pinus sylve
30	13	37.1	12	8	Q37791	Q37791 larix eural
31	13	37.1	12	8	Q37790	Q37790 larix eural
32	13	37.1	12	8	Q03815	Q03815 abies alba
33	13	37.1	12	8	Q03816	Q03816 metasequoia
34	13	37.1	12	8	Q92460	Q92460 taxus bacca
35	13	37.1	14	2	Q92842	Q92842 streptococ
36	13	37.1	15	10	Q08936	Q08936 nicotiana t
37	13	37.1	15	12	Q97090	Q97090 human immun
38	13	37.1	15	13	Q90403	Q90403 discopyge o
39	12	34.3	7	2	Q54248	Q54248 streptomyc
40	12	34.3	7	10	Q49223	Q49223 glycine max
41	12	34.3	9	12	Q70140	Q70140 human immun
42	12	34.3	10	2	P96305	P96305 alteromonas
43	12	34.3	10	2	P96423	P96423 pseudomonas
44	12	34.3	10	10	Q08938	Q08938 nicotiana t
45	12	34.3	11	2	Q52526	Q52526 plasmid sym
46	12	34.3	13	4	Q14461	Q14461 homo sapien
47	12	34.3	13	4	Q91674	Q91674 homo sapien
48	12	34.3	13	11	Q63047	Q63047 rattus norv
49	12	34.3	14	2	Q52093	Q52093 pigeon pea
50	12	34.3	14	4	P78359	P78359 homo sapien
51	12	34.3	14	4	Q16232	Q16232 homo sapien
52	12	34.3	14	5	Q26100	Q26100 pratylenchu
53	12	34.3	14	12	Q66201	Q66201 porcine tra
54	12	34.3	15	2	Q68430	Q68430 buchnera ap
55	12	34.3	15	2	Q54325	Q54325 staphylococ
56	12	34.3	15	10	Q40562	Q40562 nicotiana t
57	12	34.3	15	10	Q40563	Q40563 nicotiana t
58	12	34.3	15	11	Q92003	Q92003 rattus norv
59	12	34.3	15	12	Q97092	Q97092 human immun
60	12	34.3	15	12	Q97094	Q97094 human immun
61	11	31.4	8	2	Q921E9	Q921E9 neisseria m
62	11	31.4	9	12	Q85710	Q85710 rous sarcom
63	11	31.4	10	4	Q60912	Q60912 homo sapien
64	11	31.4	10	12	Q86580	Q86580 simian para
65	11	31.4	11	2	Q47600	Q47600 escherichia
66	11	31.4	11	2	Q47604	Q47604 escherichia
67	11	31.4	11	2	Q47569	Q47569 escherichia
68	11	31.4	11	12	P88018	P88018 human immun
69	11	31.4	11	13	Q90735	Q90735 gallus gall
70	11	31.4	13	2	Q50038	Q50038 mycobacteri
71	11	31.4	13	2	Q47601	Q47601 escherichia
72	11	31.4	13	4	Q15537	Q15537 homo sapien
73	11	31.4	13	5	Q24365	Q24365 drosophila
74	11	31.4	13	5	Q9X242	Q9X242 albinaria h
75	11	31.4	13	11	Q80517	Q80517 mus musculus
76	11	31.4	13	12	Q86129	Q86129 vesicular s
77	11	31.4	14	2	Q52840	Q52840 rhizobium l
78	11	31.4	14	2	Q921E1	Q921E1 acetobacter
79	11	31.4	14	2	Q9X715	Q9X715 campylobact
80	11	31.4	14	2	Q9W79	Q9W79 campylobact
81	11	31.4	14	12	Q84708	Q84708 porcine epi
82	11	31.4	15	2	Q54298	Q54298 salmonella
83	11	31.4	15	2	Q47892	Q47892 fremyella d
84	11	31.4	15	6	Q46661	Q46661 macropus ro
85	10	28.6	7	2	O07354	O07354 synecococc
86	10	28.6	7	11	Q63480	Q63480 rattus norv
87	10	28.6	8	2	Q68485	Q68485 klebsiella
88	10	28.6	8	4	Q15895	Q15895 homo sapien
89	10	28.6	8	5	Q15899	Q15899 babesia ovi
90	10	28.6	8	7	Q29810	Q29810 homo sapien
91	10	28.6	8	11	Q61715	Q61715 mus musculu
92	10	28.6	8	12	Q66807	Q66807 echovirus 2
93	10	28.6	9	2	Q45533	Q45533 bacillus su

095953 homo sapien  
 Q9xjn0 bacterioph  
 Q85723 simian sarc  
 Q88612 middelburg  
 Q50032 mycobacteri  
 Q26093 pisaster oc  
 Q9xs84 equus cabal

94 10 28.6 9 4 095953  
 95 10 28.6 9 9 09XJN0  
 96 10 28.6 9 12 Q85723  
 97 10 28.6 9 12 Q88612  
 98 10 28.6 10 2 Q50032  
 99 10 28.6 10 5 Q26093  
 100 10 28.6 10 6 Q9XS84

## ALIGNMENTS

RESULT 1  
 Q13695  
 ID Q13695 PRELIMINARY; PRT; 12 AA.  
 AC Q13695;  
 DT 01-NOV-1996 (TReMBLrel. 01, Created)  
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
 DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)  
 DE ACETYLCHOLINE RECEPTOR (FRAGMENT).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;  
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=THYMUS;  
 RX MEDLINE; 94071933.  
 RA MIHOVILOVIC M., MAI Y., HERBSTREITH M., RUBBOLI F., TARRONI P.,  
 RA CLEMENTI F., ROSES A.D.;  
 RT "Splicing of an anti-sense Alu sequence generates a coding sequence  
 RT variant for the alpha-3 subunit of a neuronal acetylcholine  
 RT receptor.";  
 RL Biochem. Biophys. Res. Commun. 197:137-144(1993).  
 DR EMBL; L18973; AAA86792.1; -.  
 FT NON\_TER 1  
 SQ SEQUENCE 12 AA; 1282 MW; CF969363 CRC32;

Query Match 57.1%; Score 20; DB 4; Length 12;  
 Best Local Similarity 57.1%; Pred. No. 2.5e+02;  
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VTQDDLQ 7  
 |||:|  
 DB 6 VTQNGVQ 12

RESULT 2  
 Q84179  
 ID Q84179 PRELIMINARY; PRT; 14 AA.  
 AC Q84179;  
 DT 01-NOV-1996 (TReMBLrel. 01, Created)  
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
 DT 01-NOV-1996 (TReMBLrel. 01, Last annotation update)  
 DE PROTEINASE (FRAGMENT).  
 GN 23K.  
 OS Porcine adenovirus 3.  
 OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MCCOY R.J., JOHNSON M.A., SHEPPARD M.;  
 RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U34592; AAB02184.1; -.  
 FT NON\_TER 14  
 SQ SEQUENCE 14 AA; 1582 MW; 478FF81D CRC32;

Query Match 57.1%; Score 20; DB 12; Length 14;  
 Best Local Similarity 50.0%; Pred. No. 3e+02;  
 Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 TQDDLQ 7  
 |||:|

Db 4 TEDEL 9

RESULT 3  
 Q38415 PRELIMINARY; PRT; 11 AA.  
 ID Q38415;  
 AC Q38415;  
 DT 01-NOV-1996 (TReMBLrel. 01, Created)  
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
 DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)  
 DE ANT1 PROTEIN (FRAGMENT).  
 OS Bacteriophage P7.  
 OC Viruses; dsDNA viruses, no RNA stage; Tailed phages; Myoviridae.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 90335968.  
 RA CITRON M., SCHUSTER H.;  
 RT "The c4 repressors of bacteriophages P1 and P7 are antisense RNAs.";  
 RL Cell 62:591-598(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 92319637.  
 RA CITRON M., SCHUSTER H.;  
 RT "The c4 repressor of bacteriophage P1 is a processed 77 base antisense  
 RT RNA.";  
 RL Nucleic Acids Res. 20:3085-3090(1992).  
 DR EMBL; M35139; AAA32437.1; -.  
 FT NON\_TER 11  
 SQ SEQUENCE 11 AA; 1315 MW; F2E5018A CRC32;

Query Match 54.3%; Score 19; DB 9; Length 11;  
 Best Local Similarity 50.0%; Pred. No. 3.7e+02;  
 Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VTQDDL 6  
 |||:|  
 DB 6 VTRNDI 11

RESULT 4  
 P92457  
 ID P92457 PRELIMINARY; PRT; 12 AA.  
 AC P92457;  
 DT 01-MAY-1997 (TReMBLrel. 03, Created)  
 DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)  
 DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)  
 DE CHLOROPLAST SUBUNIT OF LIGHT-INDEPENDENT PROTOCHLOROPHYLLIDE  
 DE REDUCTASE (FRAGMENT).  
 GN CHLB GENE.  
 OS Ephedra sp.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC euphyllophytes; Spermatophyta; Gnetales; Gnetales; Gnetales;  
 OC Ephedraceae; Ephedra.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 97263785.  
 RA KARPINSKA B., KARPINSKI S., HALLGREN J.E.;  
 RT "The chlB gene encoding a subunit of light-independent  
 RT protochlorophyllide reductase is edited in chloroplasts of conifers.";  
 RL Curr. Genet. 31:343-347(1997).  
 DR EMBL; X98573; CAA67182.1; -.  
 KW Chloroplast.  
 FT NON\_TER 1  
 SQ SEQUENCE 12 AA; 1441 MW; B036E488 CRC32;

Query Match 48.6%; Score 17; DB 8; Length 12;  
 Best Local Similarity 75.0%; Pred. No. 1.1e+03;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDQ 7  
Db 1 EDQ 4

RESULT 5  
ID Q53541 PRELIMINARY; PRT; 15 AA.  
AC Q53541;  
DT 01-NOV-1996 (TReMBLrel. 01, Created)  
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
DE ORF2 PROTEIN (FRAGMENT).  
OS Bacillus sp.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
OC Bacillus/Staphylococcus group; Bacillus.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 95400017.  
RA SETO Y., HASHIMOTO M., USAMI R., HAMAMOTO T., KUDO T., HORIKOSHI K.;  
RT "Characterization of a mutation responsible for an alkali-sensitive  
RT mutant, 18224, of alkaliphilic Bacillus sp. strain C-125.";  
RL Biosci. Biotechnol. Biochem. 59:1364-1368(1995).  
DR EMBL; S79441; AAB35256.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 15 AA; 1529 MW; B149434E CRC32;

Query Match 48.6%; Score 17; DB 2; Length 15;  
Best Local Similarity 40.0%; Pred. No. 1.4e+03;  
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VTQDD 5  
Db 10 IAEDD 14

RESULT 6  
ID Q15893 PRELIMINARY; PRT; 8 AA.  
AC Q15893;  
DT 01-NOV-1996 (TReMBLrel. 01, Created)  
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
DE (CLONE XP587A) (FRAGMENT).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=PLACENTA;  
RA LEE C.C., YAZDANI A., WEHNERT M., BAILEY J., COUCH L., XTONG M.,  
RA COOLBAUGH M.I., CHINAULT C.A., BALDINI A., LINDSAY E.A., ZHAO Z.Y.,  
RA CASKEY C.T.H.;  
RL Hum. Mol. Genet. 0:0-0(0).  
DR EMBL; L32073; AAA73883.1; -.  
FT NON\_TER 1  
FT NON\_TER 8  
SQ SEQUENCE 8 AA; 874 MW; 599EA97B CRC32;

Query Match 42.9%; Score 15; DB 4; Length 8;  
Best Local Similarity 50.0%; Pred. No. 2.3e+05;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 TQDDLQ 7  
Db 1 SQNPLO 6

RESULT 7  
ID Q63924 PRELIMINARY; PRT; 9 AA.

AC Q63924;  
DT 01-NOV-1996 (TReMBLrel. 01, Created)  
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)  
DE CAMP-RESPONSIVE ELEMENT MODULATOR (ALTERNATIVE PROMOTER) (FRAGMENT).  
GN CREM.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 94073967.  
RA MOLINA C.A., FOULKES N.S., LALLI E., SASSONE-CORSI P.;  
RT "Inducibility and negative autoregulation of CREM: an alternative  
RT promoter directs the expression of ICER, an early response  
RT repressor.";  
RL Cell 75:875-886(1993).  
DR EMBL; S67785; CAB32857.1; -.  
DR MGD; MGI:88495; Crem.  
FT NON\_TER 9  
SQ SEQUENCE 9 AA; 880 MW; BA9D1365 CRC32;

Query Match 42.9%; Score 15; DB 11; Length 9;  
Best Local Similarity 60.0%; Pred. No. 2.3e+05;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VTQDD 5  
Db 3 VTGDE 7

RESULT 8  
ID Q47602 PRELIMINARY; PRT; 11 AA.  
AC Q47602;  
DT 01-NOV-1996 (TReMBLrel. 01, Created)  
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)  
DE C (FRAGMENT).  
GN REASE.  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OC Escherichia.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 91139577.  
RA TAO T., BOURNE J.C., BLUMENTHAL R.M.;  
RT "A family of regulatory genes associated with type II restriction-  
RT modification systems";  
RL J. Bacteriol. 173:1367-1375(1991).  
DR EMBL; M63620; AAA24558.1; -.  
FT NON\_TER 11  
SQ SEQUENCE 11 AA; 1412 MW; BC68F8F4 CRC32;

Query Match 42.9%; Score 15; DB 2; Length 11;  
Best Local Similarity 40.0%; Pred. No. 2.7e+03;  
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VTQDD 5  
Db 1 MSRDD 5

RESULT 9  
ID Q921H4 PRELIMINARY; PRT; 14 AA.  
AC Q921H4;  
DT 01-MAY-1999 (TReMBLrel. 10, Created)  
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)  
DT 01-MAY-1999 (TReMBLrel. 10, Last annotation update)  
DE B144 PROTEIN A (FRAGMENT).

OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
RN Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
[1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 88031493.  
RA TSUGE I., SHEN F.-W.W., STEINMETZ M., BOYSE E.A.;  
RT "A gene in the H-2S:H-2D interval of the major histocompatibility  
complex which is transcribed in B cells and macrophages.";  
RL Immunogenetics 26:378-380(1987).  
DR EMBL; M18187; AAA37272.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 14 AA; 1542 MW; 607F3593 CRC32;

Query Match 42.9%; Score 15; DB 11; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 DLQ 7  
Db 3 DLQ 5

RESULT 10  
Q08947 PRELIMINARY; PRT; 15 AA.  
AC Q08947;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)  
DE DYSTROPHIN (DP1216) (FRAGMENT).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
RN Eutheria; Primates; Catarrhini; Hominidae; Homo.  
[1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 93291881.  
RA BYERS T.J., LIDOV H.G., KUNKEL L.M.;  
RT "An alternative dystrophin transcript specific to peripheral nerve.";  
RL Nat. Genet. 4:77-81(1993).  
DR EMBL; S62617; AAB27159.1; -.  
KW Structural protein; Actin-binding; Calcium-binding; Cytoskeleton;  
KW Duplication; Alternative splicing.  
FT NON\_TER 15  
SQ SEQUENCE 15 AA; 1855 MW; AE9F9478 CRC32;

Query Match 42.9%; Score 15; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 DLQ 7  
Db 11 DLQ 13

RESULT 11  
Q16387 PRELIMINARY; PRT; 15 AA.  
AC Q16387;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)  
DE MEX40 PROTEIN (FRAGMENT).  
GN MEX40.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
RN Eutheria; Primates; Catarrhini; Hominidae; Homo.  
[1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 95400293.  
RA BUDARF M.L., COLLINS J., GONG W., ROE B., WANG Z., BAILEY L.C.,

RA SELLINGER B., MICHAUD D., DRISCOLL D.A., EMANUEL B.S.;  
RT "Cloning a balanced translocation associated with DiGeorge syndrome  
and identification of a disrupted candidate gene.";  
RL Nat. Genet. 10:269-278(1995).  
DR EMBL; S79494; AAD14302.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 15 AA; 1626 MW; 746EE62B CRC32;

Query Match 42.9%; Score 15; DB 4; Length 15;  
Best Local Similarity 60.0%; Pred. No. 3.7e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 QDDLQ 7  
Db 10 RDGLQ 14

RESULT 12  
P72279 PRELIMINARY; PRT; 8 AA.  
AC P72279;  
DT 01-FEB-1997 (TrEMBLrel. 02, Created)  
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)  
DE BIPHENYL DIOXYGENASE (FRAGMENT).  
GN BPHB.  
OS Rhodococcus globerulus.  
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
OC Actinomycetales; Corynebacterineae; Nocardiaceae; Rhodococcus.  
[1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 95255652.  
RA ASTURIAS J.A., DIAZ E., TIMMIS K.N.;  
RT "The evolutionary relationship of biphenyl dioxygenase from gram-  
positive Rhodococcus globerulus P6 to multicomponent dioxygenases from  
gram-negative bacteria.";  
RL Gene 156:11-18(1995).  
DR EMBL; X80041; CAA56350.1; -.  
KW Dioxygenase.  
FT NON\_TER 8  
SQ SEQUENCE 8 AA; 989 MW; ED28AD0A CRC32;

Query Match 40.0%; Score 14; DB 2; Length 8;  
Best Local Similarity 50.0%; Pred. No. 2.3e+05;  
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 QDDL 6  
Db 4 QDEV 7

RESULT 13  
Q15902 PRELIMINARY; PRT; 8 AA.  
AC Q15902;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-AUG-1998 (TrEMBLrel. 07, Last annotation update)  
DE (CLONE XP7E7A) (FRAGMENT).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
RN Eutheria; Primates; Catarrhini; Hominidae; Homo.  
[1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=PLACENTA;  
RA LEE C.C., YAZDANI A., WEHNERT M., BAILEY J., COUCH L., XIONG M.,  
RA COOLBAUGH M.I., CHINAULT C.A., BALDINI A., LINDSAY E.A., ZHAO Z.Y.,  
RA Hum. Mol. Genet. 0:0-0(0).  
RX EMBL; L32081; AAA73892.1; -.  
FT NON\_TER 1

Db 4 EDVQ 7

RESULT 16

Q48357 PRELIMINARY; PRT; 13 AA.

ID Q48357 PRELIMINARY; PRT; 13 AA.

AC Q48357; (TREMBlrel. 01, Created)

DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)

DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)

DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)

DE TRANSCRIPTION TERMINATION FACTOR RHO (FRAGMENT).

GN RHO.

OS Escherichia coli.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC Escherichia.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE; 95129907.

RT OPPEMAN T., MARTINEZ A., RICHARDSON J.P.;

RT "The ts15 mutation of Escherichia coli alters the sequence of the C-terminal nine residues of Rho protein.";

RL Gene 152;133-134(1995).

DR ENBL; L34404; AAA68985.1; -.

GN transcription termination.

FT NON\_TER 1

SQ SEQUENCE 13 AA; 1531 MW; 43726F49 CRC32;

Query Match 40.0%; Score 14; DB 2; Length 13;

Best Local Similarity 40.0%; Pred. No. 5.1e+03;

Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 TODDL 6

DB 4 TNDEV 8

Db 4 EDVQ 7

RESULT 17

Q61340 PRELIMINARY; PRT; 13 AA.

ID Q61340 PRELIMINARY; PRT; 13 AA.

AC Q61340; (TREMBlrel. 07, Created)

DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)

DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)

DT 01-AUG-1998 (TREMBlrel. 07, Last annotation update)

DE POTASSIUM CHANNEL (FRAGMENT).

GN SHAKER.

OS Panulirus interruptus (California spiny lobster).

OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;

OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Palinura;

OC Palinuridae; Panuliridae.

RN [1]

RP SEQUENCE FROM N.A.

RA KIM M.T., BARO D.J., LANNING C.C., DOSHI M., MOSKOWITZ H., FARNHAM J.,

RA HARRIS-WARRICK R.M.;

RL Recept. Channels 0:0-0(1998).

DR ENBL; AF017135; AAC05915.1; -.

KW Ionic channel.

FT NON\_TER 13

SQ SEQUENCE 13 AA; 1336 MW; 5B640D04 CRC32;

Query Match 40.0%; Score 14; DB 5; Length 13;

Best Local Similarity 66.7%; Pred. No. 5.1e+03;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 QDD 5

DB 3 EDD 5

Db 4 EDVQ 7

RESULT 18

Q16118 PRELIMINARY; PRT; 14 AA.

ID Q16118 PRELIMINARY; PRT; 14 AA.

AC Q16118;  
DT 01-NOV-1996 (TRENBLREL. 01, Created)  
DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)  
DT 01-NOV-1998 (TRENBLREL. 08, Last annotation update)  
DE CYCLIC ADENOSINE 3',5'-MONOPHOSPHATE RESPONSE ELEMENT BINDING PROTEIN  
DE CREB [ALTERNATIVELY SPLICED, EXON W] (FRAGMENT).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 94158910.  
RA WAEBER G., MEYER T.E., LESIEUR M., HERMANN H.L., GERARD N.,  
RA HABENER J.H.;  
RT "Developmental stage-specific expression of cyclic adenosine 3',5'-  
RT monophosphate response element binding protein CREB during  
RT spermatogenesis involves alternative exon splicing.";  
RL Mol. Endocrinol. 7:1501-1501(1993).  
DR EMBL; S68577; AAB29985.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 14 AA; 1698 MW; 86068950 CRC32;

Query Match 40.0%; Score 14; DB 4; Length 14;  
Best Local Similarity 75.0%; Pred. No. 5.6e+03;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VTQD 4  
| |  
Db 5 VKQD 8

RESULT 19  
P91578  
ID P91578 PRELIMINARY; PRT; 14 AA.  
AC P91578;  
DT 01-MAY-1997 (TRENBLREL. 03, Created)  
DT 01-MAY-1997 (TRENBLREL. 03, Last sequence update)  
DT 01-AUG-1998 (TRENBLREL. 07, Last annotation update)  
DE NUCLEOSIDE TRIPHOSPHATE PHOSPHOHYDROLASE (FRAGMENT).  
GN NPH 1.  
OS Choriostroma fumiferana entomopoxvirus (CfEPV).  
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Entomopoxvirinae;  
OC Entomopoxvirus B.  
RN [1]  
RP SEQUENCE FROM N.A.  
RA LI X., BARRETT J.W., YUEN L., ARIF B.M.;  
RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U19239; AAB39411.1; -.  
KW Hydrolase.  
FT NON\_TER 1  
SQ SEQUENCE 14 AA; 1762 MW; 940E3C99 CRC32;

Query Match 40.0%; Score 14; DB 12; Length 14;  
Best Local Similarity 50.0%; Pred. No. 5.6e+03;  
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VTQD 4  
| |  
Db 9 ITND 12

RESULT 20  
O52640  
ID O52640 PRELIMINARY; PRT; 15 AA.  
AC O52640;  
DT 01-JUN-1998 (TRENBLREL. 06, Created)  
DT 01-JUN-1998 (TRENBLREL. 06, Last sequence update)  
DT 01-NOV-1998 (TRENBLREL. 08, Last annotation update)  
DE NTNU (FRAGMENT).  
GN NTNU.  
OS Pseudomonas sp.

AC Q16118;  
RN Bacteria; Proteobacteria.  
RP SEQUENCE FROM N.A.  
RC STRAIN=TW3;  
RX MEDLINE; 98215169.  
RA JAMES K.D., WILLIAMS P.A.;  
RT "ntn genes determining the early steps in the divergent catabolism of  
RT 4-nitrotoluene and toluene in Pseudomonas sp. strain TW3.";  
RL J. Bacteriol. 180:2043-2049(1998).  
DR EMBL; AF043544; AAC38356.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 15 AA; 1781 MW; FDD1B267 CRC32;

Query Match 40.0%; Score 14; DB 2; Length 15;  
Best Local Similarity 60.0%; Pred. No. 6e+03;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 QDDLQ 7  
| |  
Db 8 QSQLQ 12

RESULT 21  
Q47556  
ID Q47556 PRELIMINARY; PRT; 9 AA.  
AC Q47556;  
DT 01-NOV-1996 (TRENBLREL. 01, Created)  
DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)  
DT 01-NOV-1998 (TRENBLREL. 08, Last annotation update)  
DE ASPARTATE TRANSCARBAMOYLASE REGULATORY CHAIN (FRAGMENT).  
GN PYRI.  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OC Escherichia.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 82275057.  
RA PAUZA C.D., KARELS M.J., NAVRE M., SCHACHMAN H.K.;  
RT "Genes encoding Escherichia coli aspartate transcarbamoylase: the  
RT pyrb-pyri operon.";  
RL Proc. Natl. Acad. Sci. U.S.A. 79:4020-4024(1982).  
RN [2]  
RP SEQUENCE OF 1-5 FROM N.A.  
RX MEDLINE; 83195078.  
RA HOOVER T.A., ROOF W.D., FOLTERMANN K.F., O'DONOVAN G.A., BENCINI D.A.,  
RA WILD J.R.;  
RT "Nucleotide sequence of the structural gene (pyrB) that encodes the  
RT catalytic polypeptide of aspartate transcarbamoylase of Escherichia  
RT coli.";  
RL Proc. Natl. Acad. Sci. U.S.A. 80:2462-2466(1983).  
DR EMBL; J01670; AAA24475.1; -.  
FT NON\_TER 9  
SQ SEQUENCE 9 AA; 1085 MW; F794543D CRC32;

Query Match 37.1%; Score 13; DB 2; Length 9;  
Best Local Similarity 40.0%; Pred. No. 2.3e+05;  
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VTQDD 5  
| |  
Db 1 MTHDN 5

RESULT 22  
Q83622  
ID Q83622 PRELIMINARY; PRT; 9 AA.  
AC Q83622;  
DT 01-NOV-1996 (TRENBLREL. 01, Created)  
DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)  
DT 01-NOV-1998 (TRENBLREL. 08, Last annotation update)  
DE HYPOTHETICAL PROTEIN (FRAGMENT)).



OS Murray valley encephalitis virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
OC Flavivirus.  
RN [1]  
RX SEQUENCE FROM N.A.  
RX MEDLINE; 88118912.  
RA HAHN C.S., HAHN Y.S., RICE C.M., LEE E., DALGARNO L., STRAUSS E.G.,  
RA STRAUSS J.H.;  
RT "Conserved elements in the 3' untranslated region of flavivirus RNAs  
RT and potential cyclization sequences."  
RL J. Mol. Biol. 198;33-41(1987).  
DR EMBL; M35172; AAA66627.1; -.  
KW Hypothetical protein; Repeat.  
FT NON\_TER 1  
SQ SEQUENCE 9 AA; 1055 MW; 7EF99143 CRC32;

Query Match 37.1%; Score 13; DB 12; Length 9;  
Best Local Similarity 50.0%; Pred. No. 2.3e+05;  
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VTQD 4  
|:|  
DB 3 VSED 6

RESULT 23  
Q63056 PRELIMINARY; PRT; 10 AA.  
AC Q63056;  
DT 01-NOV-1996 (TREMELREL. 01, Created)  
DT 01-NOV-1996 (TREMELREL. 01, Last sequence update)  
DT 01-NOV-1998 (TREMELREL. 08, Last annotation update)  
DE RAT ASIALOGICOPROTEIN RECEPTOR (ASGP).  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 87026895.  
RA WATTS C.;  
RT "Isolation and expression of cDNA clones for a rat liver  
RT asialoglycoprotein receptor."  
RL Biosci. Rep. 6:527-534(1986).  
DR EMBL; M21739; AAA40763.1; -.  
SQ SEQUENCE 10 AA; 1512 MW; 0908A0D9 CRC32;

Query Match 37.1%; Score 13; DB 11; Length 10;  
Best Local Similarity 50.0%; Pred. No. 6.3e+03;  
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VTQD 4  
|:|  
DB 1 MTKD 4

RESULT 24  
Q16427 PRELIMINARY; PRT; 11 AA.  
AC Q16427;  
DT 01-NOV-1996 (TREMELREL. 01, Created)  
DT 01-NOV-1996 (TREMELREL. 01, Last sequence update)  
DT 01-MAY-1999 (TREMELREL. 10, Last annotation update)  
DE DYSTROPHIN PROTEIN (FRAGMENT).  
GN DYSTROPHIN.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 96163501.  
RA HOLDER E., MAEDA M., BIES R.D.;

RT "Expression and regulation of the dystrophin Purkinje promoter in  
RT human skeletal muscle, heart, and brain."  
RL Hum. Genet. 97:232-239(1996).  
DR EMBL; S81419; AADI4362.1; -.  
FT NON\_TER 11  
SQ SEQUENCE 11 AA; 1299 MW; AF0E38FF CRC32;

Query Match 37.1%; Score 13; DB 4; Length 11;  
Best Local Similarity 40.0%; Pred. No. 7e+03;  
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VTQDD 5  
|:|  
DB 4 VSSDE 8

RESULT 25  
O78119 PRELIMINARY; PRT; 11 AA.  
AC O78119;  
DT 01-NOV-1998 (TREMELREL. 08, Created)  
DT 01-NOV-1998 (TREMELREL. 08, Last sequence update)  
DT 01-NOV-1998 (TREMELREL. 08, Last annotation update)  
DE MHC CLASS II B LOCUS 1 (FRAGMENT).  
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;  
OC Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;  
OC Perciformes; Labroidae; Cichlidae; Oreochromis.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 98315113.  
RA MALAGA-TRILLO E., MCANDREW B., VINCEK V., ZALESKA-RUTCZYNSKA Z.,  
RA SUELTSMANN H., FIGUEROA F., KLEIN J.;  
RT "Linkage relationships and haplotype polymorphism among cichlid Mhc  
RT class II B loci."  
RL Genetics 149:1527-1547(1998).  
DR EMBL; AF050017; AAC41356.1; -.  
KW MHC.  
RP NON\_TER 1  
FT NON\_TER 11  
SQ SEQUENCE 11 AA; 1276 MW; AFCDB5B5 CRC32;

Query Match 37.1%; Score 13; DB 7; Length 11;  
Best Local Similarity 60.0%; Pred. No. 7e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VTQDD 5  
|:|  
DB 7 VTRCD 11

RESULT 26  
Q36622 PRELIMINARY; PRT; 12 AA.  
AC Q36622;  
DT 01-NOV-1996 (TREMELREL. 01, Created)  
DT 01-NOV-1996 (TREMELREL. 01, Last sequence update)  
DT 01-NOV-1996 (TREMELREL. 01, Last annotation update)  
DE CHLOROPLAST SUBUNIT OF LIGHT INDEPENDENT PROTOCHLOROPHYLLIDE  
DE REDUCTASE (FRAGMENT).  
GN CHLB.  
OS Picea abies (Norway spruce) (Picea excelsa).  
OC Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC euphyllophytes; Spermatophyta; Coniferopsida; Coniferales; Pinaceae;  
OC Picea.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX TISSUE-COTYLEDONS;  
RA KARPINSKA B., KARPINSKI S., HILGREN J.E.;  
RL Curr. Genet. 0:0-0(0).

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DR EMBL; X98685; CAA67242.1; -.
KW Chloroplast. 1 1
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1445 MW; 75FC0606 CRC32;

Query Match 37.1%; Score 13; DB 8; Length 12;
Best Local Similarity 50.0%; Pred. No. 7.7e+03;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDLQ 7
Db 1 EDLK 4

RESULT 27
Q36623 PRELIMINARY; PRT; 12 AA.
AC Q36623;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1996 (TrEMBLrel. 01, Last annotation update)
DE CHLOROPLAST SUBUNIT OF LIGHT INDEPENDENT PROTOCHLOROPHYLLIDE
DE REDUCTASE (FRAGMENT).
GN CHLB.
OS Picea abies (Norway spruce) (Picea excelsa).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Coniferopsida; Coniferales; Pinaceae;
OC Picea.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-COTYLEDONS;
RA KARPINSKA B., KARPINSKI S., HILGREN J.E.;
RL Curr. Genet. 0:0-0(0).
DR EMBL; X98685; CAA67243.1; -.
KW Chloroplast. 1 1
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1475 MW; 7337C4ED CRC32;

Query Match 37.1%; Score 13; DB 8; Length 12;
Best Local Similarity 50.0%; Pred. No. 7.7e+03;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDLQ 7
Db 1 EDLK 4

RESULT 28
Q36668 PRELIMINARY; PRT; 12 AA.
AC Q36668;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1996 (TrEMBLrel. 01, Last annotation update)
DE CHLOROPLAST SUBUNIT OF LIGHT INDEPENDENT PROTOCHLOROPHYLLIDE
DE REDUCTASE (FRAGMENT).
GN CHLB.
OS Pinus sylvestris (Scots pine).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Coniferopsida; Coniferales; Pinaceae;
OC Pinus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-COTYLEDONS;
RA KARPINSKA B., KARPINSKI S., HILGREN J.E.;
RL Curr. Genet. 0:0-0(0).
DR EMBL; X98683; CAA67240.1; -.

DR EMBL; X98685; CAA67242.1; -.
KW Chloroplast. 1 1
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1445 MW; 75FC0606 CRC32;

Query Match 37.1%; Score 13; DB 8; Length 12;
Best Local Similarity 50.0%; Pred. No. 7.7e+03;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDLQ 7
Db 1 EDLK 4

RESULT 29
Q36669 PRELIMINARY; PRT; 12 AA.
AC Q36669;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1996 (TrEMBLrel. 01, Last annotation update)
DE CHLOROPLAST SUBUNIT OF LIGHT INDEPENDENT PROTOCHLOROPHYLLIDE
DE REDUCTASE (FRAGMENT).
GN CHLB.
OS Pinus sylvestris (Scots pine).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Coniferopsida; Coniferales; Pinaceae;
OC Pinus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-COTYLEDONS;
RA KARPINSKA B., KARPINSKI S., HILGREN J.E.;
RL Curr. Genet. 0:0-0(0).
DR EMBL; X98684; CAA67241.1; -.
KW Chloroplast. 1 1
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1475 MW; 7337C4ED CRC32;

Query Match 37.1%; Score 13; DB 8; Length 12;
Best Local Similarity 50.0%; Pred. No. 7.7e+03;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDLQ 7
Db 1 EDLK 4

RESULT 30
Q37791 PRELIMINARY; PRT; 12 AA.
AC Q37791;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1996 (TrEMBLrel. 01, Last annotation update)
DE CHLOROPLAST SUBUNIT OF LIGHT INDEPENDENT PROTOCHLOROPHYLLIDE
DE REDUCTASE (FRAGMENT).
GN CHLB.
OS Larix eurolepis.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Coniferopsida; Coniferales; Pinaceae;
OC Larix.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-COTYLEDONS;
RA KARPINSKA B., KARPINSKI S., HILGREN J.E.;
RL Curr. Genet. 0:0-0(0).
DR EMBL; X98686; CAA67244.1; -.
DR EMBL; X98681; CAA67239.1; -.

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DR EMBL; X98679; CAA67237.1; -.  
KW Chloroplast.  
FT NON\_TER 1 1  
FT NON\_TER 12 12  
SQ SEQUENCE 12 AA; 1445 MW; 75FC0606 CRC32;

Query Match 37.1%; Score 13; DB 8; Length 12;  
Best Local Similarity 50.0%; Pred. No. 7.7e+03;  
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDLQ 7  
: : :  
Db 1 EDLK 4

Search completed: June 30, 2000, 16:18:45  
Job time: 7896 sec

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